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#13 Search #8 AND #5		12:50:31	1
#11 Search "Drug Design"[MeSH] OR "Crystallography, X-Ray"[MeSH]		12:49:24	41218
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☐ 1: Janes PW, Saha N, Barton WA, Kolev MV, Wimmer-Kleikamp SH, Nievergall E, Blobel CP, Himanen JP, Lackmann M, Nikolov DB.   Related Articles, Links

Adam meets Eph: an ADAM substrate recognition module acts as a molecular switch for ephrin cleavage in trans.
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Hematol Oncol Clin North Am. 2002 Oct;16(5):1125-71. Review.
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☐ 5: Baldisseri DM, Margolis JW, Weber DJ, Koo JH, Margolis FL.   Related Articles, Links

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☐ 7: Himanen JP, Rajashankar KR, Lackmann M, Cowan CA, Henkemeyer M, Nikolov DB.   Related Articles, Links

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☐ 8: Wybenga-Groot LE, Baskin B, Ong SH, Tong J, Pawson T, Sicheri F.   Related Articles, Links

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☐ 9: Thanos CD, Goodwill KE, Bowie JU.   Related Articles, Links

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☐ 10: Himanen JP, Henkemeyer M, Nikolov DB.   Related Articles, Links

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Nature. 1998 Dec 3;396(6710):486-91.
PMID: 9853759 [PubMed - indexed for MEDLINE]

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      (FILE 'HOME' ENTERED AT 14:23:12 ON 21 MAR 2006)

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                SET PLURALS ON PERM
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L1   278 S ((EPHA2 RECEPTOR) OR (EPHA2 PROTEIN) OR
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L2   3252 S ((EPHRIN? RECEPTOR?) OR (EPH? RECEPTOR?)
OR (EPH? PROTEIN?) O
L3   12679414 S (ATOMIC OR CRYSTAL? OR STRUCTUR? OR 3D OR
?DIMENSIONAL? OR ?R
L4   58 S L1 AND L3
L5   1115 S L2 AND L3
L6   49 DUP REM L4 (9 DUPLICATES REMOVED)
L7   814 DUP REM L5 (301 DUPLICATES REMOVED)

```
FSSP        FAMILIES OF STRUCTURALLY SIMILAR PROTEINS, VERSION 1.0 (Apr 1 1995)
CREATED     Tue Mar 21 16:48:01 GMT 2006 for dali on s030-014.ebi.ac.uk
METHOD      Dali ver. 2.0: Holm, L., Sander, C. (1993) J.Mol.Biol. 233,123-138
DATABASE    7062 protein chains
PDBID       6252-A
HEADER
COMPND
SOURCE
AUTHOR
SEQLENGTH   263
NALIGN      77
WARNING     pairs with Z<2.0 are structurally dissimilar
```

SUMMARY: PDB/chain identifiers and structural alignment statistics

```
  NR. STRID1 STRID2   Z   RMSD LALI LSEQ2 %IDE REVERS PERMUT NFRAG TOPO PROTEIN
    1: 6252-A 1m14-A 30.8  1.7  244   307   36     0      0      8 S
TRANSFERASE       epidermal growth factor receptor fragment
    2: 6252-A 1fmk   27.7  3.5  246   438   44     0      0      6 S
PHOSPHOTRANSFERASE       tyrosine-protein kinase src fragmen
    3: 6252-A 1b6c-B 25.0  2.7  240   326   26     0      0     15 S        COMPLEX
(ISOMERASE/PROTEIN KINASE)     fk506-binding prote
    4: 6252-A 1t53-A 22.1  2.9  223   291   27     0      0     24 S
    5: 6252-A 1hcl   21.6  3.3  234   294   21     0      0     14 S        PROTEIN
KINASE       human cyclin-dependent kinase 2 (cdk2)
    6: 6252-A 1ia8-A 21.4  2.5  222   272   22     0      0     14 S
TRANSFERASE       chk1 checkpoint kinase fragment        (homo sa
    7: 6252-A 1omw-A 21.1  2.8  237   614   21     0      0     15 S
TRANSFERASE       g-protein coupled receptor kinase 2 (grk2,
    8: 6252-A 1cdk-A 20.3  3.3  240   343   23     0      0     12 S        COMPLEX
(TRANSFERASE/INHIBITOR)       camp-dependent protein
    9: 6252-A 1wbp-A 20.2  2.8  232   350   15     0      0     18 S
TRANSFERASE       serineTHREONINE-PROTEIN KINASE SPRK1 (srpk
   10: 6252-A 2bdw-A 19.7  3.0  224   309   19     0      0     17 S
TRANSFERASE       hypothetical protein k11e8.1d fragment Mut
   11: 6252-A 1csn   19.7  3.5  233   293   17     0      0     18 S
PHOSPHOTRANSFERASE       casein kinase-1   (schizosaccharomyc
   12: 6252-A 1jwh-A 18.3  2.7  225   336   15     0      0     20 S
TRANSFERASE       casein kinase ii, alpha chain (ck ii, cat
   13: 6252-A 1zar-A 10.0  3.7  165   267   12     0      0     14 S
TRANSFERASE       rio2 kinase       (archaeoglobus fulgidus) arch
   14: 6252-A 1zao-A  9.8  3.6  164   271   12     0      0     15 S
TRANSFERASE       rio2 serine kinase       (archaeoglobus fulgidu
   15: 6252-A 1tqi-A  9.8  3.7  165   269   12     0      0     14 S        RIBOSOME
       conserved hypothetical protein (rio2)       (archa
   16: 6252-A 1ztf-A  9.5  3.4  161   243   16     0      0     19 S
TRANSFERASE       rio1 serine protein kinase       (archaeoglobus
   17: 6252-A 1j7i-A  6.6  4.9  159   260   10     0      0     23 S
TRANSFERASE       aminoglycoside 3'-phosphotransferase (aph
   18: 6252-A 1cja-A  5.2  3.8  143   327   10     0      0     17 S
TRANSFERASE       actin-fragmin kinase fragment       (physarum p
   19: 6252-A 1w2c-A  4.4  4.3  131   265    9     0      0     18 S
TRANSFERASE          inositol-trisphosphate 3-kinase a (inosito
```

```
 20: 6252-A lbol-A  4.3  4.3  136   326   10       0       0    18 S
TRANSFERASE      phosphatidylinositol phosphate kinase iibe
 21: 6252-A 2a98-A  4.0  3.7  126   259    9       0       0    15 S
TRANSFERASE      inositol 1,4,5-trisphosphate 3-kinase c fr
 22: 6252-A lia9-A  3.9  4.8  139   276   12       0       0    17 S
TRANSFERASE      transient receptor potential-related prot
 23: 6252-A lryt    3.3  4.2   78   190    5       0       0     7 S    ELECTRON
TRANSPORT   rubrerythrin biological_unit   (desu
 24: 6252-A lkny-A  3.3  9.1  111   253    9       0       0    15 S
TRANSFERASE      kanamycin nucleotidyltransferase (kntase)
 25: 6252-A 2a0b    3.1  4.3   80   118   10       0       0     7 S    SENSORY
TRANSDUCTION      hpt domain  (escherichia coli) ex
 26: 6252-A lug7-A  3.1  4.5   83   128    5       0       0     9 S
STRUCTURAL GENOMICS, UNKNOWN FUNCTION      2610208m17rik pr
 27: 6252-A lqgh-A  3.1  4.3   83   150    4       0       0    `7 S    METAL
TRANSPORT   non-heme iron-containing ferritin   (li
 28: 6252-A lzzp-A  3.0  3.5   77   109    9       0       0     7 S
TRANSFERASE      proto-oncogene tyrosine-protein kinase abl
 29: 6252-A lzuj-A  3.0  4.5   82   168    6       0       0     7 S    DNA
BINDING PROTEIN   hypothetical protein llacc01001955
 30: 6252-A lnlx-A  2.9  3.5   81   104    6       0       0     6 S    ALLERGEN .
     pollen allergen phl p 6 (phl p vi)   (phleum p
 31: 6252-A le8x-A  2.9  4.0  118   841   10       0       0    17 S
PHOSPHOINOSITIDE 3-KINASE GAMMA      phosphatidylinositol
 32: 6252-A lsr2-A  2.8  3.9   75   116    9       0       0     8 S
TRANSFERASE      putative sensor-like histidine kinase yojn
 33: 6252-A leum-A  2.8  4.2   79   161    4       0       0     7 S    METAL
BINDING PROTEIN   ferritin 1  (escherichia coli)
 34: 6252-A lbcf-A  2.8  3.8   75   157    5       0 `     0     5 S    IRON
STORAGE AND ELECTRON TRANSPORT      Bacterioferritin (
 35: 6252-A 2fha    2.7  4.1   80   172    5       0       0     8 S    IRON
STORAGE      ferritin Mutant biological_unit      (homo sa
 36: 6252-A lwn0-A  2.7  4.5   77   131   10       0       0     7 S    SIGNALING
PROTEIN      histidine-containing phosphotransfer
 37: 6252-A lozc-A  2.6  4.7  100   268    8       0       0    11 S
 38: 6252-A lorj-A  2.6  4.8   79   126    9       0       0     5 S    CHAPERONE
     flagellar protein flis   (aquifex aeolicus vf
 39: 6252-A lnsg-B  2.6  3.2   71    94    7       0       0     7 S    COMPLEX
(ISOMERASE/KINASE)      fk506-binding protein (fkbp
 40: 6252-A li5n-A  2.6  4.2   80   128    4       0       0     7 S
TRANSFERASE      chemotaxis protein chea fragment      (salmon
 41: 6252-A lhy5-A  2.6  3.6   77   120    4       0       0     7 S    TOXIN
     yersinia pestis virulence protein yope fragment
 42: 6252-A lggq-A  2.6  4.3   83   162    6       0       0     8 S    MEMBRANE
PROTEIN      outer surface protein c fragment (os
 43: 6252-A ldps-A  2.6  4.9   81   159    4       0       0     7 S    DNA-
BINDING PROTEIN   dps (pexb) Mutant biological_unit
 44: 6252-A ldd5-A  2.6  3.8   67   184    6       0       0     5 S    RIBOSOME
     ribosome recycling factor      (thermotoga mariti
 45: 6252-A 2fu2-A  2.5  2.8   55    77   15       0       0     4 S
STRUCTURAL GENOMICS, UNKNOWN FUNCTION      hypothetical pro
 46: 6252-A 2b0h-A  2.5  4.6   83   137    7       0       0     7 S
STRUCTURAL PROTEIN      talin-1 fragment  (mus musculus) mo
 47: 6252-A lz23-A  2.5  4.5   86   163    5       0       0     7 S    CELL
ADHESION   crk-associated substrate fragment (p130c
 48: 6252-A lx8z-A  2.5  4.4   70   151    3       0       0     5 S    PROTEIN
BINDING      invertasePECTIN METHYLESTERASE INHIBIT
```

```
 49: 6252-A 1rj1-A  2.5  4.1   70   148    6      0        0      6 S      PROTEIN
BINDING      invertase inhibitor     (nicotiana tabacu
 50: 6252-A 1qsp-A  2.5  3.6   78   165    5      0        0      7 S      SIGNALING
PROTEIN      ypd1 biological_unit     (saccharomyces
 51: 6252-A 1ax8    2.5  4.9   77   130    8      0        0      7 S      CYTOKINE
     obesity protein (leptin) Mutant biological_un
 52: 6252-A 1vjx-A  2.4  4.1   78   145    9      0        0      9 S
STRUCTURAL GENOMICS, UNKNOWN FUNCTION      putative ferriti
 53: 6252-A 1r72-A  2.4  2.8   57   205    4      0        0      6 S
 54: 6252-A 1j7r-A  2.4  3.7   70    77    7      0        0      6 S       METAL
BINDING PROTEIN   calcium vector protein fragment
 55: 6252-A 2cdw-A  2.3  4.6  100   408    4      0        0     11 S
 56: 6252-A 2bl7-A  2.3  2.8   57    77    2      0        0      5 S      BACTERIAL
PROTEIN      enterocine a immunity protein Mutant
 57: 6252-A 256b-A  2.3  3.4   69   106    7      0        0      6 S      ELECTRON
TRANSPORT   Cytochrome b562 (oxidized)     (escher
 58: 6252-A 1ylm-A  2.3  4.6   85   139    6      0        0      8 S
STRUCTURAL GENOMICS, UNKNOWN FUNCTION      hypothetical pro
 59: 6252-A 1oxj-A  2.3  3.3   72   170    8      0        0      7 S      RNA
BINDING PROTEIN   RNA-binding protein smaug fragment
 60: 6252-A 1ocr-C  2.3  3.9   82   261    5      0        0      7 S
OXIDOREDUCTASE     cytochrome c oxidase (ferrocytochrome c
 61: 6252-A 1m62-A  2.3  4.6   62    87    3      0        0      6 S      CHAPERONE
     bag-family molecular chaperone regulator-4 f
 62: 6252-A 1cpq    2.3  3.2   66   129    6      0        0      7 S      ELECTRON
TRANSPORT   cytochrome c'     (rhodobacter capsula
 63: 6252-A 1c17-M  2.3  4.7   81   142    9      0        0      8 S      MEMBRANE
PROTEIN      atp synthase subunit c atp synthase s
 64: 6252-A 1a48    2.3  3.1   41   298    7      0        0      6 S      ATP
BINDING PROTEIN   phosphoribosylaminoimidazole-succi
 65: 6252-A 1yux-A  2.2  4.1   81   200    5      0        0      8 S
OXIDOREDUCTASE     nigerythrin Mutant       (desulfovibrio vulg
 66: 6252-A 1w2w-A  2.2  4.2   89   207    7      0        0      8 S      ISOMERASE
     5-methylthioribose-1-phosphate isomerase fra
 67: 6252-A 1w09-A  2.2  3.6   63    92   10      0        0      6 S      CHAPERONE
     alpha-hemoglobin stabilizing protein (erythr
 68: 6252-A 1vr8-A  2.2  3.9   65   132   14      0        0      9 S      SIGNALING
PROTEIN      gtp binding regulator fragment       (the
 69: 6252-A 2ets-A  2.1  3.7   70   112    3      0        0      7 S
STRUCTURAL GENOMICS, UNKNOWN FUNCTION      hypothetical pro
 70: 6252-A 2d2s-A  2.1  4.5   78   217    9      0        0      7 S
ENDOCYTOSIS/EXOCYTOSIS  exocyst complex component exo84
 71: 6252-A 1jdc    2.1  3.3   41   418    5      0        0      6 S      HYDROLASE
     1,4-alpha maltotetrahydrolase (maltotetraose
 72: 6252-A 1fft-C  2.1  4.4   80   185    5      0        0      8 S
OXIDOREDUCTASE     ubiquinol oxidase ubiquinol oxidase ub
 73: 6252-A 1f88-A  2.1  4.7  100   338    7      0        0     11 S
SIGNALING PROTEIN      rhodopsin    bos taurus species     T.Ok
 74: 6252-A 2mhr    2.0  8.0   69   118    3      0        0      5 S      OXYGEN
BINDING     Myohemerythrin    Sipunculan worm (themis
 75: 6252-A 1mqv-A  2.0  4.2   72   123    1      0        0      6 S      ELECTRON
TRANSPORT   cytochrome c' Mutant     (rhodopseudom
 76: 6252-A 1jr8-A  2.0  3.7   75   105    8      0        0      6 S
OXIDOREDUCTASE     erv2 protein, mitochondrial fragment (
 77: 6252-A 1c3w-A  2.0  4.0   92   222    3      0        0     11 S      ION
TRANSPORT   bacteriorhodopsin (ground state wild typ
```

```
## ALIGNMENTS     1 -   30
SeqNo PDBNo AA STRUCTURE BP1 BP2  ACC OCC .   .   .   :   .   .   .   .   :   .   .   .
  .   :   .   .   .   :   .   .   .   .   :   .   .   .   .   :
    1  605 A T              0   0    0   0 .   .   .   .   .   .   .   .   .   .   .   .
  .   .   .   .   .   .   .   .   .   .   .   .   .   .
    2  606 A T       -      0   0    0   5 R   Ws  Qh  .   .   .   .   N   .   .   .   .
    3  607 A E B     -a    74  0A    0   5 Ib  Eb  Rh  .   .   .   T   .   .   .   .
                          Te
    4  608 A I       -      0   0    0  10 L   I   Th  .   .   .   L   A   .   .   .   Hh
Hh Hh Yh  .   .   .   .   Ye
    5  609 A H  >>  -       0   0    0  14 K   P   Ih  .   .   .   T   H   Fe  Fh  Ve  .   Rh
Rh Rh Kh  Lh  .   .   .   R
    6  610 A P T 34 S+      0   0    0  18 Eg  Rg  Ah  Rg  M   .   Ms  Lg  Nt  Sh  Gt  Qg  Lh
Lh Lh Lh  Kh  .   Lh
    7  611 A S T 34 S+      0   0    0  21 Tg  Eg  Rh  Sg  Et  Eg  Nt  Dg  Gt  Dh  Vt  Dg  Vh
Vh Vh Sh  Kh  .   Mh  .   Ae  .   Dg
    8  612 A C T <4 S+      0   0    0  21 Eg  Sg  Th  Ag  Nt  D   Dt  Qg  Rt  Nh  Ht  Dg  V
V  V  Ys  Lh  .   Wh  .   Ke  .   Dg
    9  613 A V E  <  -B    28  0A    0  21 Fe  Le  I   Gb  Fe  We  Fe  Fe  Ye  Ye  Ye  Y   Ds
Ds Ds Ib  Ih  .   Gh  .   Ie  .   Ve
   10  614 A T E     -B    27  0A    0  21 Ke  Re  Ve  S   Qe  De  Se  Ee  He  De  Ke  Q   Ae
Ae Ae T   Ys  .   A   .   Ee  .   Ke
   11  615 A R E     +B    26  0A    0  20 Ke  Le  Le  R   Ke  Le  Ve  Re  Ve  Ve  Ve  Lb  Ie
Ie Ie A   R   .   P   .   Fe
   12  616 A Q E     +      0   0    0  23 Ie  Ee  Qe  L   Ve  Ve  He  Ie  Ie  Ke  Ge  V   Ge
Ge Ge G   C   Ie  .   Ie  .   Le
   13  617 A K E     -B    25  0A    0  23 Ke  Ve  Ee  T   Ee  Qe  Re  Ke  Re  Ee  Re  Rb  Ke
Ke Ke G   Ve  Ee  .   Ne  .   Se
   14  618 A V E     +B    24  0A    0  23 Ve  Ke  Se  Le  Ke  Te  Ie  Te  Ke  Ee  Re  K   Le
Le Le Ve  Ke  Re  .   .   .   K
   15  619 A I E     -      0   0    0  22 Le  Le  Ie  Se  Ie  Le  Ie  Le  Le  Le  Ie  L   Me
Me Me Ie  D   S   .   S
   16  620 A G E     -B    23  0A    0  24 Ge  Ge  Ge  Ge  Ge  Ge  Ge  Ge  Ge  Ge  Ge  G   Ge
Ge Ge Se  T   E   .   D   .   M
   17  621 A A E     -B    22  0A    0  21 S   Qe  Ke  Re  Ee  E   Re  Te  We  Ke  Ee  R   Ee
Ee Ee T   .   Ks  .   .   .   Gb
   18  622 A G       -      0   0    0  22 Gt  G   Ge  Ge  G   G   G   G   G   Ge  G   G   G
G  G  G   M   Gt  .   .   .   G
   19  623 A E S   S+       0   0    0  21 At  Cs  Rt  St  Ts  At  Gs  Ss  Hs  At  Ss  Ks  Ks
Ks Ks Ks  S   .   .   .   .   Gs
   20  624 A F S   S-       0   0    0  22 Ft  Fs  Ft  Yt  Ys  Yt  Fs  Fs  Fs  Ft  Fs  Ys  Es
Es Es Es  Ps  Tt  .   .   .   Ls
   21  625 A G S   S-       0   0    0  22 Ge  G   Ge  Ge  Gs  G   G   G   S   Se  G   Se  Se
Se Se Ae  As  Es  .   .   .   Re
   22  626 A E E     -B    17  0A    0  25 Te  Ee  Ee  Se  Ve  Ee  Ee  Re  Te  Ve  Ve  Ee  Ae
Ae Ae Ne  Ke  G   S   R   .   Re
   23  627 A V E     -BC   16 39A    0  25 Ve  Ve  Ve  Le  Ve  Ve  Ve  Ve  Ve  Ve  Ie  Ve  Ve
Ve Ve Ve  Ve  Le  Fe  Fe  .   Ae
   24  628 A Y E     -BC   14 38A    0  25 Ye  We  We  Le  Ye  Qe  Ye  Me  We  Re  Fe  Fe  Fe
Fe Fe Fe  Ye  Fe  Ke  Le  .   Ve
   25  629 A K E     +BC   13 37A    0  25 Ke  Me  Re  Qs  Ke  Le  Ge  Le  Le  Re  Ee  Ee  Ne
Ne Ne Y   Ke  Fe  Ae  Te  .   Ke
   26  630 A G E     -BC   11 36A    0  26 Ge  Ge  Ge  F   Ae  Ae  Ce  Ve  Se  Ce  Ge  A   Ce
Ce Ce A   Le  Ve  A   T   .   Ve  .   Ce
   27  631 A M E     -BC   10 35A    0  26 Le  Te  Ke  Q   Re  Ve  Re  Ke  We  Ve  Te  I   Ye
Ye Ye D   Ve  Ee  Gs  Yt  .   Le  .   Ve
```

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1MQB   Images and Visualization

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Title	Crystal Structure of Ephrin A2 (ephA2) Receptor Protein Kinase
Authors	Nowakowski, J., Cronin, C.N., McRee, D.E., Knuth, M.W., Nelson, C., Pavletich, N., Rogers, J., Sang, B.C., Scheibe, D.N., Swanson, R.V., Thompson, D.A.
Primary Citation	Nowakowski, J., Cronin, C.N., McRee, D.E., Knuth, M.W., Nelson, C., Pavletich, N., Rogers, J., Sang, B.C., Scheibe, D.N., Swanson, R.V., Thompson, D.A. Structures of the Cancer Related Aurora-A, FAK and EphA2 Protein Kinases from Nanovolume Crystallography *Structure v10 pp.1659-1667, 2003* [Abstract]
History	Deposition 2002-09-16 Release 2003-09-16
Experimental Method	Type X-RAY DIFFRACTION Data N/A

Parameters

Resolution [A]	R-Value	R-Free	Space Group
2.30	0.236 (obs.)	0.288	P 3$_2$ 2 1

Unit Cell

Length [A] a 72.13 b 72.13 c 241.62

Angles [°] alpha 90.00 beta 90.00 gamma 120.00

Molecular Description Asymmetric Unit	multimer (protein homodimer (333 residues)) Polymer: 1 Molecule: **Ephrin type-A receptor 2** Fragment: **Kinase Domain** Chains: **A, B**; EC No.: 2.7.1.112
Functional Class	**Transferase**
Source	Polymer: 1 Scientific Name: **Homo sapiens** Common Name: **Human** Expression system: **Homo sapiens**

Related PDB Entries

Id	Details
1MQ4	1MQ4 IS the CRYSTAL STRUCTURE OF EPHRIN A2 (EPHA2) RECEPTOR PROTEIN
1MP8	1MP8 IS THE Crystal structure of Focal Adhesion Kinase (FAK)

Chemical Component

Identifier	Name	Formula	Drug Similarity	Ligand Structure	Ligand Interaction
ANP	PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER	$C_{10} H_{17} N_6 O_{12} P_3$	[View]	[View]	[View]

SCOP Classification (version 1.69)

Domain Info	Class	Fold	Superfamily	Family	Domain	Species
d1mqba_	Alpha and beta proteins (a+b)	Protein kinase-like (PK-like)	Protein kinase-like (PK-like)	Protein kinases, catalytic subunit	epha2 receptor tyrosine kinase	Human (Homo sapiens)
d1mqbb_	Alpha and beta proteins (a+b)	Protein kinase-like (PK-like)	Protein kinase-like (PK-like)	Protein kinases, catalytic subunit	epha2 receptor tyrosine kinase	Human (Homo sapiens)

CATH Classification (version v2.6.0)

Domain	Class	Architecture	Topology	Homology
1mqbA1	Alpha Beta	2-Layer Sandwich	Phosphorylase Kinase; domain 1	Phosphorylase Kinase; domain 1
1mqbA2	Mainly Alpha	Orthogonal Bundle	Transferase (Phosphotransferase); domain 1	Transferase (Phosphotransferase) domain 1
1mqbB1	Alpha Beta	2-Layer Sandwich	Phosphorylase Kinase; domain 1	Phosphorylase Kinase; domain 1
1mqbB2	Mainly Alpha	Orthogonal Bundle	Transferase (Phosphotransferase); domain 1	Transferase (Phosphotransferase) domain 1

GO Terms

Polymer	Molecular Function	Biological Process	Cellular Component
Ephrin type-A receptor	• protein kinase activity • protein-tyrosine kinase activity	• protein amino acid phosphorylation • transmembrane	• membrane

2 (1MQB:A, B)

- ephrin receptor activity
- ATP binding

receptor protein tyrosine kinase signaling pathway

2 (1MQB:A, B)

- ephrin receptor activity
- ATP binding

receptor protein tyrosine kinase signaling pathway

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OM protein - protein search, using sw model

Run on: March 21, 2006, 22:35:54 ; Search time 207.279 Seconds
                                            (without alignments)
                                            2068.873 Million cell updates/sec

Title: US-10-601-324-1
Perfect score: 5177
Sequence: 1 MELQAARACFALLWGCALAA.........RIAYSLLGLKDQVNTVGIPI 976

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

| | | % Query | | | | |
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3	5177	100.0	976	8	ADN03964	Adn03964 Antipsori
4	5177	100.0	976	9	ADU79818	Adu79818 Human Eph
5	5177	100.0	976	9	ADU79822	Adu79822 Human Eph
6	5177	100.0	976	9	ADV94805	Adv94805 Human ADP
7	5177	100.0	987	8	ADX97538	Adx97538 Pancreati
8	5147	99.4	976	7	ADJ95092	Adj95092 Novel NOV
9	5147	99.4	976	9	ADW96093	Adw96093 Human Eph
10	5147	99.4	976	9	ADZ66185	Adz66185 EphA2 pol
11	5147	99.4	976	9	AEB72892	Aeb72892 Human rec
12	5141	99.3	1035	9	ADZ66203	Adz66203 Protein e
13	5141	99.3	1035	9	AEB80023	Aeb80023 Human Eph
14	5141	99.3	1035	9	AEB72910	Aeb72910 Fusion pr

15	5048.5	97.5	963	8	ABM83447	Abm83447 Human dia
16	4748.5	91.7	977	9	AEA55026	Aea55026 Mouse tyr
17	4748.5	91.7	977	9	AEA55035	Aea55035 Mouse eph
18	2892	55.9	535	9	ADU79824	Adu79824 Extracell
19	2696.5	52.1	574	9	ADZ66213	Adz66213 Protein e
20	2696.5	52.1	574	9	AEB80034	Aeb80034 Human Eph
21	2696.5	52.1	574	9	AEB72921	Aeb72921 Fusion pr
22	2692	52.0	502	9	ADZ66206	Adz66206 Primary a
23	2692	52.0	502	9	AEB80026	Aeb80026 Human Eph
24	2692	52.0	502	9	AEB72913	Aeb72913 Human Eph
25	2692	52.0	563	9	ADZ66208	Adz66208 Protein e
26	2692	52.0	563	9	AEB80028	Aeb80028 Human Eph
27	2692	52.0	563	9	AEB72915	Aeb72915 Fusion pr
28	2692	52.0	581	9	ADZ66210	Adz66210 LLOss-PES
29	2692	52.0	581	9	AEB80030	Aeb80030 Human Eph
30	2692	52.0	581	9	AEB80032	Aeb80032 Human Eph
31	2692	52.0	581	9	AEB72917	Aeb72917 Fusion pr
32	2692	52.0	581	9	AEB72919	Aeb72919 Fusion pr
33	2650	51.2	991	2	AAR85090	Aar85090 EPH-like
34	2637	50.9	1037	6	ABR44241	Abr44241 Tyrosine
35	2632	50.8	1037	5	ABG61868	Abg61868 Prostate
36	2632	50.8	1037	7	ADE31683	Ade31683 Human 141
37	2629	50.8	1041	9	ADV97895	Adv97895 Murine pr
38	2622.5	50.7	953	5	ABP52826	Abp52826 Human rec
39	2604.5	50.3	975	5	ABP52827	Abp52827 Human Ehk
40	2570	49.6	998	2	AAR85092	Aar85092 EPH-like
41	2566	49.6	998	2	AAW03421	Aaw03421 Mouse dev
42	2551	49.3	1005	2	AAW83147·	Aaw83147 Rat recep
43	2519.5	48.7	986	2	AAR85091	Aar85091 EPH-like
44	2519.5	48.7	986	7	ADD46395	Add46395 Human Pro
45	2519.5	48.7	986	8	ADQ17780	Adq17780 Human sof

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OM protein - protein search, using sw model

Run on: March 21, 2006, 22:46:54 ; Search time 49.2101 Seconds
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                                  1639.734 Million cell updates/sec

Title: US-10-601-324-1
Perfect score: 5177
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                Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                              SUMMARIES

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     2   5177 100.0   976 1 US-08-702-367A-18   Sequence 18, Appl
     3   5177 100.0   976 2 US-09-949-016-6499   Sequence 6499, Ap
     4   5177 100.0   976 4 PCT-US95-04681-18   Sequence 18, Appl
     5   5147   99.4   1013 2 US-09-949-016-7991   Sequence 7991, Ap
     6 5120.5   98.9   977 1 US-08-673-789-8   Sequence 8, Appli
     7   2650   51.2   991 1 US-08-449-645A-13   Sequence 13, Appl
     8   2650   51.2   991 1 US-08-702-367A-13   Sequence 13, Appl
     9   2650   51.2   991 4 PCT-US95-04681-13   Sequence 13, Appl
    10 2634.5   50.9   967 1 US-08-449-645A-30   Sequence 30, Appl
    11 2634.5   50.9   967 1 US-08-702-367A-30   Sequence 30, Appl
    12 2622.5   50.7   953 2 US-09-751-389-7   Sequence 7, Appli
    13 2604.5   50.3   975 2 US-09-751-389-8   Sequence 8, Appli
    14   2570   49.6   998 1 US-08-449-645A-17   Sequence 17, Appl
    15   2570   49.6   998 1 US-08-702-367A-17   Sequence 17, Appl
    16   2570   49.6   998 2 US-09-949-016-6501   Sequence 6501, Ap
    17   2570   49.6   998 4 PCT-US95-04681-17   Sequence 17, Appl
    18   2570   49.6   1005 2 US-09-949-016-9901   Sequence 9901, Ap

19	2568	49.6	994	2	US-08-368-776A-12	Sequence 12, Appl
20	2566	49.6	998	2	US-08-368-776A-2	Sequence 2, Appli
21	2566	49.6	998	4	PCT-US96-00419-2	Sequence 2, Appli
22	2560.5	49.5	993	2	US-08-368-776A-11	Sequence 11, Appl
23	2551	49.3	1005	1	US-08-469-537A-103	Sequence 103, App
24	2537	49.0	982	1	US-08-673-789-4	Sequence 4, Appli
25	2532.5	48.9	986	1	US-08-673-789-3	Sequence 3, Appli
26	2520	48.7	983	1	US-08-449-645A-21	Sequence 21, Appl
27	2520	48.7	983	1	US-08-702-367A-21	Sequence 21, Appl
28	2520	48.7	983	4	PCT-US95-04681-21	Sequence 21, Appl
29	2519.5	48.7	986	1	US-08-449-645A-15	Sequence 15, Appl
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33	2518.5	48.6	983	1	US-08-162-809-16	Sequence 16, Appl
34	2518	48.6	983	2	US-09-771-161A-227	Sequence 227, App
35	2517	48.6	983	1	US-08-167-919A-10	Sequence 10, Appl
36	2517	48.6	983	2	US-08-715-106-10	Sequence 10, Appl
37	2517	48.6	983	2	US-09-442-649-10	Sequence 10, Appl
38	2514.5	48.6	968	2	US-09-751-389-6	Sequence 6, Appli
39	2512.5	48.5	1104	1	US-08-222-616-36	Sequence 36, Appl
40	2512.5	48.5	1104	2	US-08-446-648-36	Sequence 36, Appl
41	2512.5	48.5	1104	2	US-09-982-610-36	Sequence 36, Appl
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43	2463.5	47.6	1035	2	US-09-751-389-4	Sequence 4, Appli
44	2461	47.5	1036	2	US-09-751-389-2	Sequence 2, Appli
45	2387	46.1	995	1	US-08-162-809-18	Sequence 18, Appl

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OM protein - protein search, using sw model

Run on:            March 21, 2006, 23:02:20 ; Search time 167.762 Seconds
                                              (without alignments)
                                              2430.838 Million cell updates/sec

Title:            US-10-601-324-1
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Scoring table:    BLOSUM62
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Searched:         1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters:     1867569

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Post-processing: Minimum Match 0%
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                  5:  /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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        Pred. No. is the number of results predicted by chance to have a
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        and is derived by analysis of the total score distribution.
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2	5177	100.0	976	4	US-10-648-593-138	Sequence 138, App
3	5177	100.0	976	5	US-10-616-403-6	Sequence 6, Appli
4	5147	99.4	976	4	US-10-287-226-320	Sequence 320, App
5	5147	99.4	976	5	US-10-897-711-2	Sequence 2, Appli
6	2697	52.1	991	5	US-10-732-923-13667	Sequence 13667, A
7	2677	51.7	1013	5	US-10-732-923-13668	Sequence 13668, A
8	2650	51.2	991	3	US-09-823-187-44	Sequence 44, Appl
9	2632	50.8	1037	4	US-10-316-124-3	Sequence 3, Appli
10	2632	50.8	1037	4	US-10-353-690-40	Sequence 40, Appl
11	2632	50.8	1037	6	US-11-064-551-3	Sequence 3, Appli
12	2629	50.8	1041	5	US-10-840-512-215	Sequence 215, App
13	2622.5	50.7	953	4	US-10-412-277-7	Sequence 7, Appli
14	2604.5	50.3	975	4	US-10-412-277-8	Sequence 8, Appli
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16	2574	49.7	998	3	US-09-823-187-43	Sequence 43, Appl
17	2570	49.6	998	3	US-09-823-187-40	Sequence 40, Appl
18	2566	49.6	998	3	US-09-823-187-42	Sequence 42, Appl

19	2549	49.2	1005	4	US-10-029-020-63	Sequence 63, Appl
20	2542.5	49.1	993	3	US-09-823-187-39	Sequence 39, Appl
21	2542.5	49.1	993	3	US-09-823-187-41	Sequence 41, Appl
22	2522.5	48.7	983	5	US-10-732-923-13675	Sequence 13675, A
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25	2519.5	48.7	997	5	US-10-450-763-36048	Sequence 36048, A
26	2519.5	48.7	1026	5	US-10-450-763-53290	Sequence 53290, A
27	2518	48.6	983	3	US-09-771-161A-227	Sequence 227, App
28	2518	48.6	983	4	US-10-205-823-97	Sequence 97, Appl
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30	2518	48.6	983	4	US-10-295-027-602	Sequence 602, App
31	2518	48.6	983	4	US-10-029-020-59	Sequence 59, Appl
32	2518	48.6	983	6	US-11-051-454-97	Sequence 97, Appl
33	2515	48.6	983	5	US-10-794-514A-467	Sequence 467, App
34	2515	48.6	983	5	US-10-489-125B-11	Sequence 11, Appl
35	2514.5	48.6	968	4	US-10-412-277-6	Sequence 6, Appli
36	2512.5	48.5	1104	3	US-09-982-610-36	Sequence 36, Appl
37	2469.5	47.7	1130	5	US-10-840-512-216	Sequence 216, App
38	2467	47.7	1036	3	US-09-971-708-2	Sequence 2, Appli
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41	2467	47.7	1036	4	US-10-245-103-104	Sequence 104, App
42	2467	47.7	1036	4	US-10-245-107-104	Sequence 104, App
43	2467	47.7	1036	4	US-10-245-143-104	Sequence 104, App
44	2467	47.7	1036	4	US-10-245-771-104	Sequence 104, App
45	2467	47.7	1036	4	US-10-245-851-104	Sequence 104, App

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OM protein - protein search, using sw model

Run on:          March 21, 2006, 23:03:25 ; Search time 23.8594 Seconds
                                            (without alignments)
                                            1170.855 Million cell updates/sec

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Post-processing: Minimum Match 0%
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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.


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      4    5147    99.4    976   7  US-11-233-796-2         Sequence 2, Appli
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      6    5141    99.3   1035   6  US-10-966-483-20        Sequence 20, Appl
      7    5141    99.3   1035   7  US-11-021-441-4         Sequence 4, Appli
      8  2696.5    52.1    574   6  US-10-966-483-31        Sequence 31, Appl
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     11    2692    52.0    502   7  US-11-021-441-7         Sequence 7, Appli
     12    2692    52.0    563   6  US-10-966-483-25        Sequence 25, Appl
     13    2692    52.0    563   7  US-11-021-441-9         Sequence 9, Appli
     14    2692    52.0    581   6  US-10-966-483-27        Sequence 27, Appl
     15    2692    52.0    581   6  US-10-966-483-29        Sequence 29, Appl
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18	2651	51.2	1015	7	US-11-203-251A-82	Sequence 82, Appl
19	2633	50.9	1037	7	US-11-203-251A-81	Sequence 81, Appl
20	2576	49.8	985	7	US-11-113-424-61	Sequence 61, Appl
21	2570	49.6	998	7	US-11-203-251A-83	Sequence 83, Appl
22	2549	49.2	1005	7	US-11-113-424-63	Sequence 63, Appl
23	2519.5	48.7	986	7	US-11-203-251A-80	Sequence 80, Appl
24	2518	48.6	983	7	US-11-113-424-59	Sequence 59, Appl
25	2515	48.6	983	7	US-11-203-251A-78	Sequence 78, Appl
26	2466.5	47.6	1035	7	US-11-113-424-20	Sequence 20, Appl
27	2457	47.5	1052	7	US-11-113-424-22	Sequence 22, Appl
28	2392	46.2	976	7	US-11-203-251A-76	Sequence 76, Appl
29	2387	46.1	995	7	US-11-113-424-62	Sequence 62, Appl
30	2375.5	45.9	1005	7	US-11-203-251A-84	Sequence 84, Appl
31	2370	45.8	987	6	US-10-770-726-61	Sequence 61, Appl
32	2370	45.8	987	7	US-11-203-251A-87	Sequence 87, Appl
33	2364	45.7	456	6	US-10-966-483-34	Sequence 34, Appl
34	2364	45.7	456	7	US-11-021-441-18	Sequence 18, Appl
35	2357.5	45.5	1055	7	US-11-072-175-139	Sequence 139, App
36	2357.5	45.5	1055	7	US-11-203-251A-86	Sequence 86, Appl
37	2356.5	45.5	1055	7	US-11-169-041-155	Sequence 155, App
38	2356.5	45.5	1055	7	US-11-051-720-1417	Sequence 1417, Ap
39	2318	44.8	984	7	US-11-113-424-60	Sequence 60, Appl
40	2312	44.7	984	7	US-11-203-251A-85	Sequence 85, Appl
41	2281.5	44.1	998	7	US-11-203-251A-88	Sequence 88, Appl
42	2265.5	43.8	998	6	US-10-510-524-1	Sequence 1, Appli
43	2195	42.4	490	6	US-10-966-483-42	Sequence 42, Appl
44	2195	42.4	490	7	US-11-021-441-26	Sequence 26, Appl
45	2179	42.1	479	6	US-10-966-483-36	Sequence 36, Appl

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OM protein - protein search, using sw model

Run on: March 21, 2006, 22:41:59 ; Search time 41.0084 Seconds
                                             (without alignments)
                                             2289.959 Million cell updates/sec

Title: US-10-601-324-1
Perfect score: 5177
Sequence: 1 MELQAARACFALLWGCALAA.........RIAYSLLGLKDQVNTVGIPI 976

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_80:*
                1: pir1:*
                2: pir2:*
                3: pir3:*
                4: pir4:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5177	100.0	976	2	A36355	protein-tyrosine k
2	4748.5	91.7	977	2	S49004	tyrosine kinase Mp
3	4589.5	88.7	975	2	I48974	receptor-protein t
4	2677	51.7	1013	2	I50615	receptor-type prot
5	2650	51.2	991	2	I78843	receptor protein-t
6	2576	49.8	985	2	I51549	receptor tyrosine
7	2571	49.7	981	2	S51604	receptor-like tyro
8	2570	49.6	998	2	I58351	receptor protein-t
9	2566	49.6	998	2	JC5672	receptor tyrosine
10	2549	49.2	1005	2	S49015	receptor tyrosine
11	2524.5	48.8	986	2	S78059	protein-tyrosine k
12	2522.5	48.7	983	2	B45583	receptor tyrosine
13	2519.5	48.7	986	2	I78844	receptor protein-t
14	2518	48.6	983	2	A38224	protein-tyrosine k
15	2491	48.1	983	2	A45583	receptor tyrosine
16	2387	46.1	995	2	A56599	embryo kinase 5 -
17	2349.5	45.4	970	2	I78842	receptor protein-t
18	2336.5	45.1	948	2	S51605	receptor-like tyro
19	2322	44.9	984	1	A34076	protein-tyrosine k
20	2318	44.8	984	2	A39753	protein-tyrosine k

21	2295.5	44.3	988	2	I50611	protein-tyrosine k
22	2285	44.1	898	2	S47489	receptor tyrosine
23	2283	44.1	893	2	S51603	receptor-like tyro
24	2272	43.9	993	2	I48653	mouse developmenta
25	2265.5	43.8	998	2	S37627	protein-tyrosine k
26	2245	43.4	849	2	I50617	protein-tyrosine k
27	2212.5	42.7	985	2	I51672	receptor tyrosine
28	2193	42.4	877	2	I48967	brain-specific kin
29	2179.5	42.1	938	2	I49071	protein kinase - m
30	2148.5	41.5	952	2	I50612	protein-tyrosine k
31	2135	41.2	426	2	I48759	protein-tyrosine k
32	2133	41.2	987	2	A54092	protein-tyrosine k
33	2112	40.8	987	2	I48652	mouse developmenta
34	2091.5	40.4	987	2	I48953	eph-related recept
35	1796.5	34.7	1006	2	JC5526	kinase-defective E
36	1667.5	32.2	1019	2	T13039	tyrosine kinase re
37	1416	27.4	490	2	I50613	protein-tyrosine k
38	1390.5	26.9	612	2	S33506	protein-tyrosine k
39	1365	26.4	1122	2	T42400	Eph receptor tyros
40	1364.5	26.4	480	2	I48760	protein-tyrosine k
41	1342	25.9	478	2	A57174	protein-tyrosine k
42	1248.5	24.1	610	2	I48612	developmental kina
43	1248.5	24.1	626	2	I48614	developmental kina
44	1243	24.0	605	2	JC5673	receptor tyrosine
45	1241	24.0	919	2	T29581	hypothetical prote

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OM protein - protein search, using sw model

Run on: March 21, 2006, 22:37:09 ; Search time 217.717 Seconds
                                          (without alignments)
                                          3162.796 Million cell updates/sec

Title: US-10-601-324-1
Perfect score: 5177
Sequence: 1 MELQAARACFALLWGCALAA..........RIAYSLLGLKDQVNTVGIPI 976

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   UniProt_05.80:*
                 1: uniprot_sprot:*
                 2: uniprot_trembl:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                                   SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID		Description
1	5177	100.0	976	1	EPHA2_HUMAN	P29317	homo sapien
2	5147	99.4	976	2	Q8N3Z2_HUMAN	Q8n3z2	homo sapien
3	4748.5	91.7	977	1	EPHA2_MOUSE	Q03145	mus musculu
4	3765.5	72.7	974	2	Q6DII4_XENTR	Q6dii4	xenopus tro
5	3747.5	72.4	976	2	Q6NTV5_XENLA	Q6ntv5	xenopus lae
6	3738.5	72.2	963	2	Q5FWW9_XENLA	Q5fww9	xenopus lae
7	3673	70.9	977	2	Q9PWR5_XENLA	Q9pwr5	xenopus lae
8	2819.5	54.5	984	2	Q6NZS1_BRARE	Q6nzs1	brachydanio
9	2738.5	52.9	1042	2	Q4RXA0_TETNG	Q4rxa0	tetraodon n
10	2677	51.7	1013	1	EPHA5_CHICK	P54755	gallus gall
11	2632	50.8	1037	1	EPHA5_HUMAN	P54756	homo sapien
12	2592	50.1	969	2	Q7Z3F2_HUMAN	Q7z3f2	homo sapien
13	2583.5	49.9	986	2	Q7ZYM7_XENLA	Q7zym7	xenopus lae
14	2582.5	49.9	986	1	EPA4A_XENLA	Q91845	xenopus lae
15	2576	49.8	985	1	EPA4B_XENLA	Q91694	xenopus lae
16	2574	49.7	998	1	EPHA7_RAT	P54759	rattus norv
17	2573	49.7	994	2	Q8R381_MOUSE	Q8r381	mus musculu
18	2571	49.7	998	2	Q8BSU8_MOUSE	Q8bsu8	mus musculu
19	2569	49.6	998	1	EPHA7_HUMAN	Q15375	homo sapien
20	2566	49.6	998	1	EPHA7_MOUSE	Q61772	mus musculu
21	2565.5	49.6	1017	2	Q59FT4_HUMAN	Q59ft4	homo sapien
22	2554	49.3	969	2	Q98TD0_CHICK	Q98td0	gallus gall

23	2549	49.2	1005	1	EPHA5_RAT	P54757	rattus norv
24	2542.5	49.1	993	1	EPHA7_CHICK	042422	gallus gall
25	2530.5	48.9	986	2	Q5ZEW1_BRARE	Q5zew1	brachydanio
26	2529.5	48.9	984	2	Q8BRB1_MOUSE	Q8brb1	mus musculu
27	2529.5	48.9	984	2	Q8C3U1_MOUSE	Q8c3u1	mus musculu
28	2529.5	48.9	986	2	Q80VZ2_MOUSE	Q80vz2	mus musculu
29	2524.5	48.8	986	1	EPHA4_CHICK	Q07496	gallus gall
30	2524.5	48.8	986	1	EPHA4_MOUSE	Q03137	mus musculu
31	2522.5	48.7	983	1	EPHA3_CHICK	P29318	gallus gall
32	2519.5	48.7	986	1	EPHA4_HUMAN	P54764	homo sapien
33	2518	48.6	983	1	EPHA3_HUMAN	P29320	homo sapien
34	2517.5	48.6	984	1	EPHA3_RAT	008680	rattus norv
35	2511	48.5	983	2	Q6P4R6_HUMAN	Q6p4r6	homo sapien
36	2491	48.1	983	1	EPHA3_MOUSE	P29319	mus musculu
37	2470.5	47.7	949	2	Q58F15_HUMAN	Q58f15	homo sapien
38	2463.5	47.6	1035	1	EPHA6_MOUSE	Q62413	mus musculu
39	2452	47.4	927	2	Q99KA8_MOUSE	Q99ka8	mus musculu
40	2427.5	46.9	981	1	EPHA3_BRARE	013146	brachydanio
41	2398	46.3	976	1	EPHA1_HUMAN	P21709	homo sapien
42	2396.5	46.3	977	1	EPHA1_MOUSE	Q60750	mus musculu
43	2390.5	46.2	977	2	Q6IR19_MOUSE	Q6ir19	mus musculu
44	2375.5	45.9	1005	1	EPHA8_HUMAN	P29322	homo sapien
45	2373	45.8	1004	1	EPHB2_CHICK	P28693	gallus gall

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OM protein - protein search, using sw model

Run on: March 21, 2006, 23:07:20 ; Search time 187 Seconds
                                            (without alignments)
                                            655.544 Million cell updates/sec

Title: US-10-601-324-1_COPY_605_883
Perfect score: 279
Sequence: 1 TTEIHPSCVTRQKVIGAGEF..........FADIVSILDKLIRAPDSLKT 279

Scoring table: OLIGO
                 Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size :   0

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   A_Geneseq_21:*
                 1: geneseqp1980s:*
                 2: geneseqp1990s:*
                 3: geneseqp2000s:*
                 4: geneseqp2001s:*
                 5: geneseqp2002s:*
                 6: geneseqp2003as:*
                 7: geneseqp2003bs:*
                 8: geneseqp2004s:*
                 9: geneseqp2005s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	279	100.0	456	9	ADZ66216	Adz66216 Primary a
2	279	100.0	456	9	AEB80037	Aeb80037 Human Eph
3	279	100.0	456	9	AEB72924	Aeb72924 Human Eph
4	279	100.0	479	9	ADZ66218	Adz66218 Protein e
5	279	100.0	479	9	AEB80039	Aeb80039 Human Eph
6	279	100.0	479	9	AEB72926	Aeb72926 Fusion pr
7	279	100.0	490	9	ADZ66223	Adz66223 Protein e
8	279	100.0	490	9	AEB80045	Aeb80045 Human Eph
9	279	100.0	490	9	AEB72932	Aeb72932 Fusion pr
10	279	100.0	497	9	ADZ66220	Adz66220 Protein e
11	279	100.0	497	9	AEB80043	Aeb80043 Human Eph
12	279	100.0	497	9	AEB80041	Aeb80041 Human Eph
13	279	100.0	497	9	AEB72928	Aeb72928 Fusion pr
14	279	100.0	497	9	AEB72930	Aeb72930 Fusion pr
15	279	100.0	963	8	ABM83447	Abm83447 Human dia

16	279	100.0	976	7	ADE40423	Ade40423 Human eph
17	279	100.0	976	7	ADJ95092	Adj95092 Novel NOV
18	279	100.0	976	8	ADL61214	Adl61214 Human pro
19	279	100.0	976	8	ADN03964	Adn03964 Antipsori
20	279	100.0	976	9	ADU79818	Adu79818 Human Eph
21	279	100.0	976	9	ADU79822	Adu79822 Human Eph
22	279	100.0	976	9	ADV94805	Adv94805 Human ADP
23	279	100.0	976	9	ADW96093	Adw96093 Human Eph
24	279	100.0	976	9	ADZ66185	Adz66185 EphA2 pol
25	279	100.0	976	9	AEB72892	Aeb72892 Human rec
26	279	100.0	987	8	ADX97538	Adx97538 Pancreati
27	279	100.0	1035	9	ADZ66203	Adz66203 Protein e
28	279	100.0	1035	9	AEB80023	Aeb80023 Human Eph
29	279	100.0	1035	9	AEB72910	Aeb72910 Fusion pr
30	77	27.6	977	9	AEA55026	Aea55026 Mouse tyr
31	77	27.6	977	9	AEA55035	Aea55035 Mouse eph
32	55	19.7	55	6	ABU83030	Abu83030 Human rec
33	36	12.9	308	7	ADA39525	Ada39525 Human kin
34	36	12.9	308	8	ADS18041	Ads18041 Human nov
35	36	12.9	334	7	ADF12512	Adf12512 Consensus
36	36	12.9	534	8	ADX91454	Adx91454 Plant ful
37	36	12.9	558	8	ADX91452	Adx91452 Plant ful
38	36	12.9	942	7	ADA39523	Ada39523 Human kin
39	36	12.9	942	8	ADS18039	Ads18039 Human nov
40	36	12.9	948	2	AAW83148	Aaw83148 Rat recep
41	36	12.9	948	5	ABP52824	Abp52824 Rat recep
42	36	12.9	1035	5	ABG70391	Abg70391 Human Eph
43	36	12.9	1035	5	ABP52823	Abp52823 Mouse rec
44	36	12.9	1035	7	ADF12510	Adf12510 Murine Ep
45	36	12.9	1036	4	AAG67398	Aag67398 Amino aci

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OM protein - protein search, using sw model

Run on: March 21, 2006, 23:15:00 ; Search time 48 Seconds
                                            (without alignments)
                                            480.552 Million cell updates/sec

Title: US-10-601-324-1_COPY_605_883
Perfect score: 279
Sequence: 1 TTEIHPSCVTRQKVIGAGEF..........FADIVSILDKLIRAPDSLKT 279

Scoring table: OLIGO
                 Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size :   0

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   Issued_Patents_AA:*
                 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
                 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
                 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
                 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	279	100.0	976	1	US-08-449-645A-18	Sequence 18, Appl
2	279	100.0	976	1	US-08-702-367A-18	Sequence 18, Appl
3	279	100.0	976	2	US-09-949-016-6499	Sequence 6499, Ap
4	279	100.0	976	4	PCT-US95-04681-18	Sequence 18, Appl
5	279	100.0	1013	2	US-09-949-016-7991	Sequence 7991, Ap
6	173	62.0	977	1	US-08-673-789-8	Sequence 8, Appli
7	55	19.7	55	1	US-08-456-647B-42	Sequence 42, Appl
8	55	19.7	55	1	US-08-237-401A-42	Sequence 42, Appl
9	54	19.4	54	1	US-08-469-537A-29	Sequence 29, Appl
10	38	13.6	687	1	US-08-449-645A-29	Sequence 29, Appl
11	38	13.6	687	1	US-08-702-367A-29	Sequence 29, Appl
12	36	12.9	308	2	US-10-004-542-4	Sequence 4, Appli
13	36	12.9	308	2	US-10-430-797-4	Sequence 4, Appli
14	36	12.9	942	2	US-10-004-542-2	Sequence 2, Appli
15	36	12.9	942	2	US-10-430-797-2	Sequence 2, Appli
16	36	12.9	948	1	US-08-469-537A-101	Sequence 101, App
17	36	12.9	948	2	US-09-751-389-5	Sequence 5, Appli
18	36	12.9	1035	2	US-09-751-389-4	Sequence 4, Appli

19	36	12.9	1036	2	US-09-751-389-2	Sequence 2, Appli
20	30	10.8	397	2	US-09-949-016-11445	Sequence 11445, A
21	30	10.8	612	1	US-08-673-789-11	Sequence 11, Appl
22	30	10.8	945	2	US-09-949-016-8172	Sequence 8172, Ap
23	30	10.8	951	1	US-08-162-809-2	Sequence 2, Appli
24	30	10.8	970	1	US-08-673-789-7	Sequence 7, Appli
25	30	10.8	970	1	US-08-449-645A-11	Sequence 11, Appl
26	30	10.8	970	1	US-08-702-367A-11	Sequence 11, Appl
27	30	10.8	970	4	PCT-US95-04681-11	Sequence 11, Appl
28	30	10.8	973	1	US-08-162-809-8	Sequence 8, Appli
29	30	10.8	973	1	US-08-162-809-10	Sequence 10, Appl
30	30	10.8	984	1	US-08-673-789-6	Sequence 6, Appli
31	30	10.8	984	2	US-09-949-016-6502	Sequence 6502, Ap
32	30	10.8	988	1	US-08-162-809-14	Sequence 14, Appl
33	30	10.8	993	1	US-08-348-143-1	Sequence 1, Appli
34	30	10.8	993	1	US-08-571-785-1	Sequence 1, Appli
35	30	10.8	993	2	US-09-192-435-1	Sequence 1, Appli
36	30	10.8	993	2	US-09-558-340-1	Sequence 1, Appli
37	30	10.8	994	2	US-08-542-635-2	Sequence 2, Appli
38	30	10.8	995	1	US-08-162-809-18	Sequence 18, Appl
39	30	10.8	995	1	US-08-673-789-5	Sequence 5, Appli
40	30	10.8	998	1	US-08-449-645A-20	Sequence 20, Appl
41	30	10.8	998	1	US-08-702-367A-20	Sequence 20, Appl
42	30	10.8	998	4	PCT-US95-04681-20	Sequence 20, Appl
43	30	10.8	1011	1	US-08-162-809-12	Sequence 12, Appl
44	29	10.4	993	2	US-08-368-776A-11	Sequence 11, Appl
45	29	10.4	994	2	US-08-368-776A-12	Sequence 12, Appl

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OM protein - protein search, using sw model

Run on:          March 21, 2006, 23:16:40 ; Search time 163 Seconds
                                            (without alignments)
                                            715.180 Million cell updates/sec

Title:           US-10-601-324-1_COPY_605_883
Perfect score:   279
Sequence:        1 TTEIHPSCVTRQKVIGAGEF..........FADIVSILDKLIRAPDSLKT 279

Scoring table:   OLIGO
                 Gapop 60.0 , Gapext 60.0

Searched:        1867569 seqs, 417829326 residues

Word size :      0

Total number of hits satisfying chosen parameters:      1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :       Published_Applications_AA_Main:*
                 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
                 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
                 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
                 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
                 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
                 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

          Pred. No. is the number of results predicted by chance to have a
          score greater than or equal to the score of the result being printed,
          and is derived by analysis of the total score distribution.
```

                                   SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	279	100.0	976	4	US-10-366-288-2	Sequence 2, Appli
2	279	100.0	976	4	US-10-287-226-320	Sequence 320, App
3	279	100.0	976	4	US-10-648-593-138	Sequence 138, App
4	279	100.0	976	5	US-10-616-403-6	Sequence 6, Appli
5	279	100.0	976	5	US-10-897-711-2	Sequence 2, Appli
6	124	44.4	297	5	US-10-794-493-15	Sequence 15, Appl
7	55	19.7	55	3	US-09-158-722-42	Sequence 42, Appl
8	36	12.9	308	4	US-10-430-797-4	Sequence 4, Appli
9	36	12.9	308	4	US-10-843-129-4	Sequence 4, Appli
10	36	12.9	334	3	US-09-971-708-5	Sequence 5, Appli
11	36	12.9	337	5	US-10-794-493-16	Sequence 16, Appl
12	36	12.9	534	4	US-10-425-114-54118	Sequence 54118, A
13	36	12.9	558	4	US-10-425-114-54116	Sequence 54116, A
14	36	12.9	942	4	US-10-430-797-2	Sequence 2, Appli
15	36	12.9	942	4	US-10-843-129-2	Sequence 2, Appli
16	36	12.9	948	4	US-10-412-277-5	Sequence 5, Appli
17	36	12.9	976	5	US-10-732-923-13613	Sequence 13613, A
18	36	12.9	1035	3	US-09-971-708-3	Sequence 3, Appli

19	36	12.9	1035	4	US-10-412-277-4	Sequence 4, Appli
20	36	12.9	1035	4	US-10-029-020-20	Sequence 20, Appl
21	36	12.9	1036	3	US-09-971-708-2	Sequence 2, Appli
22	36	12.9	1036	4	US-10-245-752-104	Sequence 104, App
23	36	12.9	1036	4	US-10-245-859-104	Sequence 104, App
24	36	12.9	1036	4	US-10-245-103-104	Sequence 104, App
25	36	12.9	1036	4	US-10-245-107-104	Sequence 104, App
26	36	12.9	1036	4	US-10-245-143-104	Sequence 104, App
27	36	12.9	1036	4	US-10-245-771-104	Sequence 104, App
28	36	12.9	1036	4	US-10-245-851-104	Sequence 104, App
29	36	12.9	1036	4	US-10-245-883-104	Sequence 104, App
30	36	12.9	1036	4	US-10-237-535-104	Sequence 104, App
31	36	12.9	1036	4	US-10-238-183-104	Sequence 104, App
32	36	12.9	1036	4	US-10-238-283-104	Sequence 104, App
33	36	12.9	1036	4	US-10-238-370-104	Sequence 104, App
34	36	12.9	1036	4	US-10-245-055-104	Sequence 104, App
35	36	12.9	1036	4	US-10-245-147-104	Sequence 104, App
36	36	12.9	1036	4	US-10-245-730-104	Sequence 104, App
37	36	12.9	1036	4	US-10-245-739-104	Sequence 104, App
38	36	12.9	1036	4	US-10-246-210-104	Sequence 104, App
39	36	12.9	1036	4	US-10-239-196-104	Sequence 104, App
40	36	12.9	1036	4	US-10-243-024-104	Sequence 104, App
41	36	12.9	1036	4	US-10-243-409-104	Sequence 104, App
42	36	12.9	1036	4	US-10-245-621-104	Sequence 104, App
43	36	12.9	1036	4	US-10-245-880-104	Sequence 104, App
44	36	12.9	1036	4	US-10-245-033-104	Sequence 104, App
45	36	12.9	1036	4	US-10-243-095-104	Sequence 104, App

```
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OM protein - protein search, using sw model

Run on:          March 21, 2006, 23:29:01 ; Search time 23 Seconds
                                            (without alignments)
                                            347.208 Million cell updates/sec

Title:           US-10-601-324-1_COPY_605_883
Perfect score:   279
Sequence:        1 TTEIHPSCVTRQKVIGAGEF..........FADIVSILDKLIRAPDSLKT 279


Scoring table:   OLIGO
                 Gapop 60.0 , Gapext 60.0

Searched:        169630 seqs, 28622889 residues

Word size :      0

Total number of hits satisfying chosen parameters:       169630

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :       Published_Applications_AA_New:*
                 1:  /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
                 2:  /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
                 3:  /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
                 4:  /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
                 5:  /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
                 6:  /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
                 7:  /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
                 8:  /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	279	100.0	456	6	US-10-966-483-34	Sequence 34, Appl
2	279	100.0	456	7	US-11-021-441-18	Sequence 18, Appl
3	279	100.0	479	6	US-10-966-483-36	Sequence 36, Appl
4	279	100.0	479	7	US-11-021-441-20	Sequence 20, Appl
5	279	100.0	490	6	US-10-966-483-42	Sequence 42, Appl
6	279	100.0	490	7	US-11-021-441-26	Sequence 26, Appl
7	279	100.0	497	6	US-10-966-483-38	Sequence 38, Appl
8	279	100.0	497	6	US-10-966-483-40	Sequence 40, Appl
9	279	100.0	497	7	US-11-021-441-22	Sequence 22, Appl
10	279	100.0	497	7	US-11-021-441-24	Sequence 24, Appl
11	279	100.0	976	6	US-10-966-483-2	Sequence 2, Appli
12	279	100.0	976	6	US-10-511-273-1	Sequence 1, Appli
13	279	100.0	976	7	US-11-233-796-2	Sequence 2, Appli
14	279	100.0	976	7	US-11-072-175-138	Sequence 138, App
15	279	100.0	976	7	US-11-203-251A-77	Sequence 77, Appl

16	279	100.0	1035	6	US-10-966-483-20	Sequence 20, Appl
17	279	100.0	1035	7	US-11-021-441-4	Sequence 4, Appli
18	36	12.9	1035	7	US-11-113-424-20	Sequence 20, Appl
19	36	12.9	1052	7	US-11-113-424-22	Sequence 22, Appl
20	30	10.8	984	7	US-11-113-424-60	Sequence 60, Appl
21	30	10.8	984	7	US-11-203-251A-85	Sequence 85, Appl
22	30	10.8	987	6	US-10-770-726-61	Sequence 61, Appl
23	30	10.8	987	7	US-11-203-251A-87	Sequence 87, Appl
24	30	10.8	995	7	US-11-113-424-62	Sequence 62, Appl
25	30	10.8	998	6	US-10-510-524-1	Sequence 1, Appli
26	30	10.8	998	7	US-11-203-251A-88	Sequence 88, Appl
27	30	10.8	1055	7	US-11-169-041-155	Sequence 155, App
28	30	10.8	1055	7	US-11-072-175-139	Sequence 139, App
29	30	10.8	1055	7	US-11-203-251A-86	Sequence 86, Appl
30	30	10.8	1055	7	US-11-051-720-1417	Sequence 1417, Ap
31	29	10.4	998	7	US-11-203-251A-83	Sequence 83, Appl
32	28	10.0	987	6	US-10-949-720-395	Sequence 395, App
33	28	10.0	987	7	US-11-203-251A-89	Sequence 89, Appl
34	28	10.0	990	6	US-10-821-234-1201	Sequence 1201, Ap
35	25	9.0	985	7	US-11-113-424-61	Sequence 61, Appl
36	25	9.0	986	7	US-11-203-251A-80	Sequence 80, Appl
37	23	8.2	983	7	US-11-113-424-59	Sequence 59, Appl
38	23	8.2	983	7	US-11-203-251A-78	Sequence 78, Appl
39	23	8.2	1005	7	US-11-113-424-63	Sequence 63, Appl
40	23	8.2	1015	7	US-11-203-251A-82	Sequence 82, Appl
41	23	8.2	1037	7	US-11-203-251A-81	Sequence 81, Appl
42	20	7.2	1005	7	US-11-203-251A-84	Sequence 84, Appl
43	15	5.4	15	6	US-10-966-483-16	Sequence 16, Appl
44	15	5.4	976	7	US-11-203-251A-76	Sequence 76, Appl
45	12	4.3	1124	7	US-11-195-197-9	Sequence 9, Appli

```
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OM protein - protein search, using sw model

Run on:          March 21, 2006, 23:11:05 ; Search time 40 Seconds
                                            (without alignments)
                                            671.112 Million cell updates/sec

Title:           US-10-601-324-1_COPY_605_883
Perfect score:   279
Sequence:        1 TTEIHPSCVTRQKVIGAGEF..........FADIVSILDKLIRAPDSLKT 279

Scoring table:   OLIGO
                 Gapop 60.0 , Gapext 60.0

Searched:        283416 seqs, 96216763 residues

Word size :      0

Total number of hits satisfying chosen parameters:      283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :       PIR_80:*
                 1:  pir1:*
                 2:  pir2:*
                 3:  pir3:*
                 4:  pir4:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                   SUMMARIES
```

Result No.	Score	% Query Match	Length	DB	ID	Description
1	279	100.0	976	2	A36355	protein-tyrosine k
2	77	27.6	426	2	I48759	protein-tyrosine k
3	77	27.6	975	2	I48974	receptor-protein t
4	77	27.6	977	2	S49004	tyrosine kinase Mp
5	36	12.9	334	2	T43450	hypothetical prote
6	36	12.9	948	2	S51605	receptor-like tyro
7	30	10.8	84	2	A24910	probable tyrosine
8	30	10.8	275	2	I48761	protein-tyrosine k
9	30	10.8	478	2	A57174	protein-tyrosine k
10	30	10.8	480	2	I48760	protein-tyrosine k
11	30	10.8	612	2	S33506	protein-tyrosine k
12	30	10.8	938	2	I49071	protein kinase - m
13	30	10.8	952	2	I50612	protein-tyrosine k
14	30	10.8	970	2	I78842	receptor protein-t
15	30	10.8	984	2	A39753	protein-tyrosine k
16	30	10.8	985	2	I51672	receptor tyrosine
17	30	10.8	988	2	I50611	protein-tyrosine k
18	30	10.8	993	2	I48653	mouse developmenta
19	30	10.8	995	2	A56599	embryo kinase 5 -
20	30	10.8	998	2	S37627	protein-tyrosine k

21	29	10.4	998	2	I58351	receptor protein-t
22	29	10.4	998	2	JC5672	receptor tyrosine
23	28	10.0	987	2	A54092	protein-tyrosine k
24	28	10.0	987	2	I48652	mouse developmenta
25	28	10.0	987	2	I48953	eph-related recept
26	25	9.0	849	2	I50617	protein-tyrosine k
27	25	9.0	985	2	I51549	receptor tyrosine
28	25	9.0	986	2	I78844	receptor protein-t
29	25	9.0	986	2	S78059	protein-tyrosine k
30	23	8.2	55	2	PT0186	protein-tyrosine k
31	23	8.2	57	2	S35727	protein-tyrosine k
32	23	8.2	490	2	I50613	protein-tyrosine k
33	23	8.2	877	2	I48967	brain-specific kin
34	23	8.2	893	2	S51603	receptor-like tyro
35	23	8.2	898	2	S47489	receptor tyrosine
36	23	8.2	981	2	S51604	receptor-like tyro
37	23	8.2	983	2	B45583	receptor tyrosine
38	23	8.2	983	2	A38224	protein-tyrosine k
39	23	8.2	983	2	A45583	receptor tyrosine
40	23	8.2	991	2	I78843	receptor protein-t
41	23	8.2	1005	2	S49015	receptor tyrosine
42	23	8.2	1013	2	I50615	receptor-type prot
43	19	6.8	57	2	PT0193	protein-tyrosine k
44	19	6.8	57	2	PT0188	protein-tyrosine k
45	19	6.8	57	2	PT0187	protein-tyrosine k

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OM protein - protein search, using sw model

Run on: March 21, 2006, 23:07:50 ; Search time 231 Seconds
                                            (without alignments)
                                            852.132 Million cell updates/sec

Title: US-10-601-324-1_COPY_605_883
Perfect score: 279
Sequence: 1 TTEIHPSCVTRQKVIGAGEF..........FADIVSILDKLIRAPDSLKT 279

Scoring table: OLIGO
                  Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size :   0

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   UniProt_05.80:*
                  1: uniprot_sprot:*
                  2: uniprot_trembl:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	279	100.0	976	1	EPHA2_HUMAN	P29317 homo sapien
2	279	100.0	976	2	Q8N3Z2_HUMAN	Q8n3z2 homo sapien
3	160	57.3	253	2	Q96HF4_HUMAN	Q96hf4 homo sapien
4	77	27.6	977	1	EPHA2_MOUSE	Q03145 mus musculu
5	55	19.7	55	2	Q90ZJ1_CHICK	Q90zj1 gallus gall
6	52	18.6	963	2	Q5FWW9_XENLA	Q5fww9 xenopus lae
7	52	18.6	974	2	Q6DII4_XENTR	Q6dii4 xenopus tro
8	52	18.6	976	2	Q6NTV5_XENLA	Q6ntv5 xenopus lae
9	52	18.6	977	2	Q9PWR5_XENLA	Q9pwr5 xenopus lae
10	48	17.2	57	2	Q91999_XENLA	Q91999 xenopus lae.
11	36	12.9	328	2	Q4T461_TETNG	Q4t461 tetraodon n
12	36	12.9	334	2	Q9UF33_HUMAN	Q9uf33 homo sapien
13	36	12.9	356	2	Q4T7X3_TETNG	Q4t7x3 tetraodon n
14	36	12.9	639	2	Q8CCN2_MOUSE	Q8ccn2 mus musculu
15	36	12.9	948	1	EPHA6_RAT	P54758 rattus norv
16	36	12.9	963	2	Q4RQW0_TETNG	Q4rqw0 tetraodon n
17	36	12.9	976	2	Q90ZN9_BRARE	Q90zn9 brachydanio
18	36	12.9	1006	2	Q4RV12_TETNG	Q4rv12 tetraodon n
19	36	12.9	1035	1	EPHA6_MOUSE	Q62413 mus musculu
20	36	12.9	1072	2	Q4SWL0_TETNG	Q4swl0 tetraodon n
21	32	11.5	780	2	Q4SQX3_TETNG	Q4sqx3 tetraodon n
22	31	11.1	536	2	Q70W06_CIOIN	Q70w06 ciona intes

23	31	11.1	1006	2	Q4H3M7_CIOIN	Q4h3m7 ciona intes
24	30	10.8	84	2	Q7LZG9_CHICK	Q7lzg9 gallus gall
25	30	10.8	88	2	Q4RDZ6_TETNG	Q4rdz6 tetraodon n
26	30	10.8	179	2	Q4TFI7_TETNG	Q4tfi7 tetraodon n
27	30	10.8	570	2	Q4S771_TETNG	Q4s771 tetraodon n
28	30	10.8	885	2	Q4RVA1_TETNG	Q4rva1 tetraodon n
29	30	10.8	902	1	EPB1B_XENLA	Q91736 xenopus lae
30	30	10.8	938	2	Q60669_MOUSE	Q60669 mus musculu
31	30	10.8	943	2	Q8CBE2_MOUSE	Q8cbe2 mus musculu
32	30	10.8	946	2	Q5TFU3_HUMAN	Q5tfu3 homo sapien
33	30	10.8	950	2	Q4SP88_TETNG	Q4sp88 tetraodon n
34	30	10.8	972	2	Q5T0U6_HUMAN	Q5t0u6 homo sapien
35	30	10.8	974	1	EPHB3_XENLA	Q91735 xenopus lae
36	30	10.8	974	2	Q6DFG4_XENLA	Q6dfg4 xenopus lae
37	30	10.8	974	2	Q6NRE9_XENLA	Q6nre9 xenopus lae
38	30	10.8	984	1	EPHB1_CHICK	Q07494 gallus gall
39	30	10.8	984	1	EPHB1_HUMAN	P54762 homo sapien
40	30	10.8	984	1	EPHB1_RAT	P09759 rattus norv
41	30	10.8	984	2	Q8CBF3_MOUSE	Q8cbf3 mus musculu
42	30	10.8	984	2	Q6PG23_MOUSE	Q6pg23 mus musculu
43	30	10.8	985	1	EPB1A_XENLA	Q91571 xenopus lae
44	30	10.8	987	2	Q5T0U8_HUMAN	Q5t0u8 homo sapien
45	30	10.8	988	1	EPHB3_CHICK	Q07498 gallus gall

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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 21, 2006, 23:29:51 ; Search time 36.1 Seconds
                                            (without alignments)
                                            2227.322 Million cell updates/sec

Title: US-10-601-324-2
Perfect score: 1741
Sequence: 1 gaccccaaccaggctgtgtt..........ggctccccagcacgagcggc 915

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 4886326

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10601324/runat_21032006_124020_20217/app_query.fasta_1
-DB=A_Geneseq -QFMT=fastan -SUFFIX=n2p.rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p
-USER=US10601324_@CGN_1_1_348_@runat_21032006_124020_20217 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   A_Geneseq_21:*
                 1: geneseqp1980s:*
                 2: geneseqp1990s:*
                 3: geneseqp2000s:*
                 4: geneseqp2001s:*
                 5: geneseqp2002s:*
                 6: geneseqp2003as:*
                 7: geneseqp2003bs:*
                 8: geneseqp2004s:*
                 9: geneseqp2005s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                     %
Result   Query
  No.   Score   Match Length DB   ID   Description

1	1590	91.3	456	9	ADZ66216	Adz66216 Primary a
2	1590	91.3	456	9	AEB80037	Aeb80037 Human Eph
3	1590	91.3	456	9	AEB72924	Aeb72924 Human Eph
4	1590	91.3	479	9	ADZ66218	Adz66218 Protein e
5	1590	91.3	479	9	AEB80039	Aeb80039 Human Eph
6	1590	91.3	479	9	AEB72926	Aeb72926 Fusion pr
7	1590	91.3	490	9	ADZ66223	Adz66223 Protein e
8	1590	91.3	490	9	AEB80045	Aeb80045 Human Eph
9	1590	91.3	490	9	AEB72932	Aeb72932 Fusion pr
10	1590	91.3	497	9	ADZ66220	Adz66220 Protein e
11	1590	91.3	497	9	AEB80043	Aeb80043 Human Eph
12	1590	91.3	497	9	AEB80041	Aeb80041 Human Eph
13	1590	91.3	497	9	AEB72928	Aeb72928 Fusion pr
14	1590	91.3	497	9	AEB72930	Aeb72930 Fusion pr
15	1590	91.3	963	8	ABM83447	Abm83447 Human dia
16	1590	91.3	976	7	ADE40423	Ade40423 Human eph
17	1590	91.3	976	7	ADJ95092	Adj95092 Novel NOV
18	1590	91.3	976	8	ADL61214	Adl61214 Human pro
19	1590	91.3	976	8	ADN03964	Adn03964 Antipsori
20	1590	91.3	976	9	ADU79818	Adu79818 Human Eph
21	1590	91.3	976	9	ADU79822	Adu79822 Human Eph
22	1590	91.3	976	9	ADV94805	Adv94805 Human ADP
23	1590	91.3	976	9	ADW96093	Adw96093 Human Eph
24	1590	91.3	976	9	ADZ66185	Adz66185 EphA2 pol
25	1590	91.3	976	9	AEB72892	Aeb72892 Human rec
26	1590	91.3	987	8	ADX97538	Adx97538 Pancreati
27	1590	91.3	1035	9	ADZ66203	Adz66203 Protein e
28	1590	91.3	1035	9	AEB80023	Aeb80023 Human Eph
29	1590	91.3	1035	9	AEB72910	Aeb72910 Fusion pr
30	1544	88.7	977	9	AEA55026	Aea55026 Mouse tyr
31	1544	88.7	977	9	AEA55035	Aea55035 Mouse eph
32	1194.5	68.6	710	2	AAR75714	Aar75714 Eph-relat
33	1194.5	68.6	722	2	AAR75705	Aar75705 Eph-relat
34	1194.5	68.6	744	2	AAR75713	Aar75713 Eph-relat
35	1192.5	68.5	877	2	AAW71628	Aaw71628 Mouse Bsk
36	1192.5	68.5	1041	9	ADV97895	Adv97895 Murine pr
37	1189.5	68.3	953	5	ABP52826	Abp52826 Human rec
38	1189.5	68.3	975	5	ABP52827	Abp52827 Human Ehk
39	1189.5	68.3	991	2	AAR85090	Aar85090 EPH-like
40	1189.5	68.3	1037	5	ABG61868	Abg61868 Prostate
41	1189.5	68.3	1037	6	ABR44241	Abr44241 Tyrosine
42	1189.5	68.3	1037	7	ADE31683	Ade31683 Human 141
43	1184.5	68.0	928	2	AAR97853	Aar97853 Rat REK7
44	1177.5	67.6	1005	2	AAW83147	Aaw83147 Rat recep
45	1156.5	66.4	849	2	AAR75706	Aar75706 Eph-relat

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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 21, 2006, 23:45:21 ; Search time 8.1 Seconds
                                           (without alignments)
                                           1867.858 Million cell updates/sec

Title: US-10-601-324-2
Perfect score: 1741
Sequence: 1 gaccccaaccaggctgtgtt..........ggctccccagcacgagcggc 915

Scoring table: BLOSUM62
                  Xgapop 10.0 , Xgapext 0.5
                  Ygapop 10.0 , Ygapext 0.5
                  Fgapop 6.0 , Fgapext 7.0
                  Delop   6.0 , Delext   7.0

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 1144120

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10601324/runat_21032006_124025_20308/app_query.fasta_1
-DB=Issued_Patents_AA -QFMT=fastan -SUFFIX=n2p.rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss02p -USER=US10601324_@CGN_1_1_71_@runat_21032006_124025_20308
-NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Issued_Patents_AA:*
                  1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
                  2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
                  3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
                  4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                  5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                  6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                            SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1590	91.3	976	1	US-08-449-645A-18	Sequence 18, Appl
2	1590	91.3	976	1	US-08-702-367A-18	Sequence 18, Appl
3	1590	91.3	976	2	US-09-949-016-6499	Sequence 6499, Ap

4	1590	91.3	976	4	PCT-US95-04681-18	Sequence 18, Appl
5	1590	91.3	1013	2	US-09-949-016-7991	Sequence 7991, Ap
6	1569	90.1	977	1	US-08-673-789-8	Sequence 8, Appli
7	1194.5	68.6	490	1	US-08-673-789-13	Sequence 13, Appl
8	1194.5	68.6	710	1	US-08-162-809-22	Sequence 22, Appl
9	1194.5	68.6	722	1	US-08-162-809-4	Sequence 4, Appli
10	1194.5	68.6	744	1	US-08-162-809-20	Sequence 20, Appl
11	1192.5	68.5	877	1	US-08-673-789-2	Sequence 2, Appli
12	1189.5	68.3	953	2	US-09-751-389-7	Sequence 7, Appli
13	1189.5	68.3	967	1	US-08-449-645A-30	Sequence 30, Appl
14	1189.5	68.3	967	1	US-08-702-367A-30	Sequence 30, Appl
15	1189.5	68.3	975	2	US-09-751-389-8	Sequence 8, Appli
16	1189.5	68.3	991	1	US-08-449-645A-13	Sequence 13, Appl
17	1189.5	68.3	991	1	US-08-702-367A-13	Sequence 13, Appl
18	1189.5	68.3	991	4	PCT-US95-04681-13	Sequence 13, Appl
19	1184.5	68.0	928	1	US-08-442-248-2	Sequence 2, Appli
20	1184.5	68.0	928	1	US-08-440-815-2	Sequence 2, Appli
21	1184.5	68.0	928	2	US-08-486-449-2	Sequence 2, Appli
22	1184.5	68.0	928	2	US-08-578-684-2	Sequence 2, Appli
23	1177.5	67.6	1005	1	US-08-469-537A-103	Sequence 103, App
24	1156.5	66.4	849	1	US-08-162-809-6	Sequence 6, Appli
25	1156.5	66.4	986	1	US-08-673-789-3	Sequence 3, Appli
26	1154.5	66.3	849	1	US-08-673-789-10	Sequence 10, Appl
27	1152.5	66.2	986	1	US-08-449-645A-15	Sequence 15, Appl
28	1152.5	66.2	986	1	US-08-702-367A-15	Sequence 15, Appl
29	1152.5	66.2	986	4	PCT-US95-04681-15	Sequence 15, Appl
30	1152.5	66.2	997	2	US-09-949-016-7171	Sequence 7171, Ap
31	1152.5	66.2	1104	1	US-08-222-616-36	Sequence 36, Appl
32	1152.5	66.2	1104	2	US-08-446-648-36	Sequence 36, Appl
33	1152.5	66.2	1104	2	US-09-982-610-36	Sequence 36, Appl
34	1152.5	66.2	1104	4	PCT-US95-04228-36	Sequence 36, Appl
35	1151.5	66.1	968	2	US-09-751-389-6	Sequence 6, Appli
36	1151.5	66.1	983	1	US-08-162-809-16	Sequence 16, Appl
37	1149.5	66.0	982	1	US-08-673-789-4	Sequence 4, Appli
38	1149.5	66.0	983	1	US-08-449-645A-21	Sequence 21, Appl
39	1149.5	66.0	983	1	US-08-702-367A-21	Sequence 21, Appl
40	1149.5	66.0	983	2	US-09-771-161A-227	Sequence 227, App
41	1149.5	66.0	983	4	PCT-US95-04681-21	Sequence 21, Appl
42	1146.5	65.9	983	1	US-08-167-919A-10	Sequence 10, Appl
43	1146.5	65.9	983	2	US-08-715-106-10	Sequence 10, Appl
44	1146.5	65.9	983	2	US-09-442-649-10	Sequence 10, Appl
45	1143.5	65.7	998	1	US-08-449-645A-17	Sequence 17, Appl

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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 22, 2006, 00:04:02 ; Search time 34.1 Seconds
                                              (without alignments)
                                              2242.310 Million cell updates/sec

Title: US-10-601-324-2
Perfect score: 1741
Sequence: 1 gaccccaaccaggctgtgtt..........ggctccccagcacgagcggc 915

Scoring table: BLOSUM62
               Xgapop 10.0 , Xgapext 0.5
               Ygapop 10.0 , Ygapext 0.5
               Fgapop 6.0 , Fgapext 7.0
               Delop   6.0 , Delext   7.0

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 3735138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10601324/runat_21032006_124031_20479/app_query.fasta_1
-DB=Published_Applications_AA_Main -QFMT=fastan -SUFFIX=n2p.rapbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p
-USER=US10601324_@CGN_1_1_307_@runat_21032006_124031_20479 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Published_Applications_AA_Main:*
               1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
               2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
               3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
               4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
               5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
               6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

          Pred. No. is the number of results predicted by chance to have a
          score greater than or equal to the score of the result being printed,
          and is derived by analysis of the total score distribution.

                              SUMMARIES

               %
Result   Query
   No.   Score Match Length DB ID   Description
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     1   1590   91.3   976   4 US-10-366-288-2   Sequence 2, Appli
     2   1590   91.3   976   4 US-10-287-226-320   Sequence 320, App

3	1590	91.3	976	4	US-10-648-593-138	Sequence 138, App
4	1590	91.3	976	5	US-10-616-403-6	Sequence 6, Appli
5	1590	91.3	976	5	US-10-897-711-2	Sequence 2, Appli
6	1523.5	87.5	297	5	US-10-794-493-15	Sequence 15, Appl
7	1194.5	68.6	490	5	US-10-732-923-13669	Sequence 13669, A
8	1194.5	68.6	827	5	US-10-732-923-13666	Sequence 13666, A
9	1194.5	68.6	991	5	US-10-732-923-13667	Sequence 13667, A
10	1194.5	68.6	1013	5	US-10-732-923-13668	Sequence 13668, A
11	1192.5	68.5	1041	5	US-10-840-512-215	Sequence 215, App
12	1189.5	68.3	369	5	US-10-732-923-13681	Sequence 13681, A
13	1189.5	68.3	953	4	US-10-412-277-7	Sequence 7, Appli
14	1189.5	68.3	975	4	US-10-412-277-8	Sequence 8, Appli
15	1189.5	68.3	991	3	US-09-823-187-44	Sequence 44, Appl
16	1189.5	68.3	1037	4	US-10-316-124-3	Sequence 3, Appli
17	1189.5	68.3	1037	4	US-10-353-690-40	Sequence 40, Appl
18	1189.5	68.3	1037	6	US-11-064-551-3	Sequence 3, Appli
19	1185.5	68.1	295	5	US-10-794-493-13	Sequence 13, Appl
20	1184.5	68.0	928	2	US-08-578-684-2	Sequence 2, Appli
21	1177.5	67.6	1005	4	US-10-029-020-63	Sequence 63, Appl
22	1152.5	66.2	295	5	US-10-794-493-12	Sequence 12, Appl
23	1152.5	66.2	985	4	US-10-029-020-61	Sequence 61, Appl
24	1152.5	66.2	986	5	US-10-723-860-597	Sequence 597, App
25	1152.5	66.2	986	5	US-10-756-149-4880	Sequence 4880, Ap
26	1152.5	66.2	997	5	US-10-450-763-36048	Sequence 36048, A
27	1152.5	66.2	1026	5	US-10-450-763-53290	Sequence 53290, A
28	1152.5	66.2	1104	3	US-09-982-610-36	Sequence 36, Appl
29	1151.5	66.1	968	4	US-10-412-277-6	Sequence 6, Appli
30	1151.5	66.1	983	5	US-10-732-923-13675	Sequence 13675, A
31	1149.5	66.0	983	3	US-09-771-161A-227	Sequence 227, App
32	1149.5	66.0	983	4	US-10-205-823-97	Sequence 97, Appl
33	1149.5	66.0	983	4	US-10-345-680-2	Sequence 2, Appli
34	1149.5	66.0	983	4	US-10-295-027-602	Sequence 602, App
35	1149.5	66.0	983	4	US-10-029-020-59	Sequence 59, Appl
36	1149.5	66.0	983	5	US-10-794-514A-467	Sequence 467, App
37	1149.5	66.0	983	5	US-10-489-125B-11	Sequence 11, Appl
38	1149.5	66.0	983	6	US-11-051-454-97	Sequence 97, Appl
39	1147.5	65.9	295	5	US-10-794-493-11	Sequence 11, Appl
40	1143.5	65.7	295	5	US-10-794-493-6	Sequence 6, Appli
41	1143.5	65.7	295	5	US-10-794-493-9	Sequence 9, Appli
42	1143.5	65.7	993	3	US-09-823-187-39	Sequence 39, Appl
43	1143.5	65.7	993	3	US-09-823-187-41	Sequence 41, Appl
44	1143.5	65.7	998	3	US-09-823-187-40	Sequence 40, Appl
45	1142.5	65.6	295	5	US-10-794-493-8	Sequence 8, Appli

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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 22, 2006, 00:05:47 ; Search time 3.6 Seconds
                                             (without alignments)
                                             1454.997 Million cell updates/sec

Title: US-10-601-324-2
Perfect score: 1741
Sequence: 1 gaccccaaccaggctgtgtt..........ggctccccagcacgagcggc 915

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 169630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 339260

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10601324/runat_21032006_124034_20541/app_query.fasta_1
-DB=Published_Applications_AA_New -QFMT=fastan -SUFFIX=n2p.rapbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss02p
-USER=US10601324_@CGN_1_1_17_@runat_21032006_124034_20541 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Published_Applications_AA_New:*
                 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
                 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
                 3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
                 4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
                 5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
                 6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
                 7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
                 8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result   Query
   No.   Score Match Length DB   ID   Description

1	1590	91.3	456	6	US-10-966-483-34	Sequence 34, Appl
2	1590	91.3	456	7	US-11-021-441-18	Sequence 18, Appl
3	1590	91.3	479	6	US-10-966-483-36	Sequence 36, Appl
4	1590	91.3	479	7	US-11-021-441-20	Sequence 20, Appl
5	1590	91.3	490	6	US-10-966-483-42	Sequence 42, Appl
6	1590	91.3	490	7	US-11-021-441-26	Sequence 26, Appl
7	1590	91.3	497	6	US-10-966-483-38	Sequence 38, Appl
8	1590	91.3	497	6	US-10-966-483-40	Sequence 40, Appl
9	1590	91.3	497	7	US-11-021-441-22	Sequence 22, Appl
10	1590	91.3	497	7	US-11-021-441-24	Sequence 24, Appl
11	1590	91.3	976	6	US-10-966-483-2	Sequence 2, Appli
12	1590	91.3	976	6	US-10-511-273-1	Sequence 1, Appli
13	1590	91.3	976	7	US-11-233-796-2	Sequence 2, Appli
14	1590	91.3	976	7	US-11-072-175-138	Sequence 138, App
15	1590	91.3	976	7	US-11-203-251A-77	Sequence 77, Appl
16	1590	91.3	1035	6	US-10-966-483-20	Sequence 20, Appl
17	1590	91.3	1035	7	US-11-021-441-4	Sequence 4, Appli
18	1189.5	68.3	1015	7	US-11-203-251A-82	Sequence 82, Appl
19	1189.5	68.3	1037	7	US-11-203-251A-81	Sequence 81, Appl
20	1177.5	67.6	1005	7	US-11-113-424-63	Sequence 63, Appl
21	1152.5	66.2	985	7	US-11-113-424-61	Sequence 61, Appl
22	1152.5	66.2	986	7	US-11-203-251A-80	Sequence 80, Appl
23	1149.5	66.0	983	7	US-11-113-424-59	Sequence 59, Appl
24	1149.5	66.0	983	7	US-11-203-251A-78	Sequence 78, Appl
25	1143.5	65.7	998	7	US-11-203-251A-83	Sequence 83, Appl
26	1117.5	64.2	984	7	US-11-203-251A-85	Sequence 85, Appl
27	1114.5	64.0	984	7	US-11-113-424-60	Sequence 60, Appl
28	1106.5	63.6	987	6	US-10-770-726-61	Sequence 61, Appl
29	1106.5	63.6	987	7	US-11-203-251A-87	Sequence 87, Appl
30	1106.5	63.6	1055	7	US-11-169-041-155	Sequence 155, App
31	1106.5	63.6	1055	7	US-11-072-175-139	Sequence 139, App
32	1106.5	63.6	1055	7	US-11-203-251A-86	Sequence 86, Appl
33	1106.5	63.6	1055	7	US-11-051-720-1417	Sequence 1417, Ap
34	1105.5	63.5	995	7	US-11-113-424-62	Sequence 62, Appl
35	1090.5	62.6	1035	7	US-11-113-424-20	Sequence 20, Appl
36	1090.5	62.6	1052	7	US-11-113-424-22	Sequence 22, Appl
37	1087.5	62.5	998	6	US-10-510-524-1	Sequence 1, Appli
38	1087.5	62.5	998	7	US-11-203-251A-88	Sequence 88, Appl
39	1043.5	59.9	1005	7	US-11-203-251A-84	Sequence 84, Appl
40	1038.5	59.6	987	6	US-10-949-720-395	Sequence 395, App
41	1038.5	59.6	987	7	US-11-203-251A-89	Sequence 89, Appl
42	1038.5	59.6	990	6	US-10-821-234-1201	Sequence 1201, Ap
43	970	55.7	976	7	US-11-203-251A-76	Sequence 76, Appl
44	770.5	44.3	1006	7	US-11-203-251A-90	Sequence 90, Appl
45	620.5	35.6	258	6	US-10-877-346-75	Sequence 75, Appl

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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 21, 2006, 23:36:36 ; Search time 8.9 Seconds
                                            (without alignments)
                                            1978.390 Million cell updates/sec

Title: US-10-601-324-2
Perfect score: 1741
Sequence: 1 gaccccaaccaggctgtgtt..........ggctccccagcacgagcggc 915

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10601324/runat_21032006_124023_20268/app_query.fasta_1
-DB=PIR -QFMT=fastan -SUFFIX=n2p.rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p
-USER=US10601324_@CGN_1_1_63_@runat_21032006_124023_20268 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   PIR_80:*
                 1: pir1:*
                 2: pir2:*
                 3: pir3:*
                 4: pir4:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                   %
Result   Query
  No.   Score   Match Length DB ID   Description
----
    1   1590   91.3   976   2 A36355   protein-tyrosine k
    2   1551   89.1   426   2 I48759   protein-tyrosine k
    3   1544   88.7   977   2 S49004   tyrosine kinase Mp
    4   1519   87.2   975   2 I48974   receptor-protein t
    5   1194.5   68.6   490   2 I50613   protein-tyrosine k

6	1194.5	68.6	1013	2	I50615	receptor-type prot
7	1192.5	68.5	877	2	I48967	brain-specific kin
8	1189.5	68.3	991	2	I78843	receptor protein-t
9	1184.5	68.0	898	2	S47489	receptor tyrosine
10	1177.5	67.6	893	2	S51603	receptor-like tyro
11	1177.5	67.6	981	2	S51604	receptor-like tyro
12	1177.5	67.6	1005	2	S49015	receptor tyrosine
13	1156.5	66.4	849	2	I50617	protein-tyrosine k
14	1153.5	66.3	986	2	S78059	protein-tyrosine k
15	1152.5	66.2	985	2	I51549	receptor tyrosine
16	1152.5	66.2	986	2	I78844	receptor protein-t
17	1151.5	66.1	983	2	B45583	receptor tyrosine
18	1149.5	66.0	983	2	A38224	protein-tyrosine k
19	1143.5	65.7	998	2	I58351	receptor protein-t
20	1135.5	65.2	998	2	JC5672	receptor tyrosine
21	1121.5	64.4	983	2	A45583	receptor tyrosine
22	1114.5	64.0	984	2	A39753	protein-tyrosine k
23	1111.5	63.8	952	2	I50612	protein-tyrosine k
24	1106.5	63.6	480	2	I48760	protein-tyrosine k
25	1105.5	63.5	995	2	A56599	embryo kinase 5 -
26	1103.5	63.4	478	2	A57174	protein-tyrosine k
27	1102.5	63.3	970	2	I78842	receptor protein-t
28	1091.5	62.7	948	2	S51605	receptor-like tyro
29	1088.5	62.5	988	2	I50611	protein-tyrosine k
30	1088	62.5	985	2	I51672	receptor tyrosine ·
31	1087.5	62.5	998	2	S37627	protein-tyrosine k
32	1083.5	62.2	993	2	I48653	mouse developmenta
33	1049.5	60.3	938	2	I49071	protein kinase - m
34	1044.5	60.0	612	2	S33506	protein-tyrosine k
35	1038.5	59.6	987	2	A54092	protein-tyrosine k
36	1035.5	59.5	987	2	I48953	eph-related recept
37	1029.5	59.1	987	2	I48652	mouse developmenta
38	994.5	57.1	372	2	S23363	protein-tyrosine k
39	974	55.9	1019	2	T13039	tyrosine kinase re
40	941	54.0	984	1	A34076	protein-tyrosine k
41	793.5	45.6	919	2	T29581	hypothetical prote
42	781	44.9	1122	2	T42400	Eph receptor tyros
43	770.5	44.3	1006	2	JC5526	kinase-defective E
44	724	41.6	275	2	I48761	protein-tyrosine k
45	633.5	36.4	334	2	T43450	hypothetical prote

```
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```

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 21, 2006, 23:30:21 ; Search time 50.6 Seconds
                                               (without alignments)
                                               2551.614 Million cell updates/sec

Title: US-10-601-324-2
Perfect score: 1741
Sequence: 1 gaccccaaccaggctgtgtt.........ggctccccagcacgagcggc 915

Scoring table: BLOSUM62
                  Xgapop 10.0 , Xgapext   0.5
                  Ygapop 10.0 , Ygapext   0.5
                  Fgapop   6.0 , Fgapext   7.0
                  Delop   6.0 , Delext   7.0

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 4332886

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                        Maximum Match 100%
                        Listing first 45 summaries

```
Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10601324/runat_21032006_124022_20229/app_query.fasta_1
-DB=UniProt -QFMT=fastan -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p
-USER=US10601324_@CGN_1_1_466_@runat_21032006_124022_20229 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

Database :   UniProt_05.80:*
                  1:   uniprot_sprot:*
                  2:   uniprot_trembl:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1590	91.3	976	1	EPHA2_HUMAN	P29317 homo sapien
2	1590	91.3	976	2	Q8N3Z2_HUMAN	Q8n3z2 homo sapien
3	1544	88.7	977	1	EPHA2_MOUSE	Q03145 mus musculu
4	1424.5	81.8	974	2	Q6DII4_XENTR	Q6dii4 xenopus tro
5	1412.5	81.1	963	2	Q5FWW9_XENLA	Q5fww9 xenopus lae
6	1407.5	80.8	976	2	Q6NTV5_XENLA	Q6ntv5 xenopus lae
7	1355	77.8	977	2	Q9PWR5_XENLA	Q9pwr5 xenopus lae

8	1309.5	75.2	712	2	Q4SC90_TETNG	Q4sc90 tetraodon n
9	1274.5	73.2	1042	2	Q4RXA0_TETNG	Q4rxa0 tetraodon n
10	1246.5	71.6	666	2	O73876_BRARE	O73876 brachydanio
11	1246.5	71.6	984	2	Q6NZS1_BRARE	Q6nzs1 brachydanio
12	1194.5	68.6	1013	1	EPHA5_CHICK	P54755 gallus gall
13	1192.5	68.5	877	1	EPHA5_MOUSE	Q60629 mus musculu
14	1189.5	68.3	369	2	Q95K57_MACFA	Q95k57 macaca fasc
15	1189.5	68.3	819	2	Q6PFV6_MOUSE	Q6pfv6 mus musculu
16	1189.5	68.3	1017	2	Q59FT4_HUMAN	Q59ft4 homo sapien
17	1189.5	68.3	1037	1	EPHA5_HUMAN	P54756 homo sapien
18	1181.5	67.9	969	2	Q7Z3F2_HUMAN	Q7z3f2 homo sapien
19	1177.5	67.6	1005	1	EPHA5_RAT	P54757 rattus norv
20	1156.5	66.4	986	1	EPHA4_CHICK	Q07496 gallus gall
21	1153.5	66.3	927	2	Q99KA8_MOUSE	Q99ka8 mus musculu
22	1153.5	66.3	986	1	EPHA4_MOUSE	Q03137 mus musculu
23	1153.5	66.3	986	2	Q80VZ2_MOUSE	Q80vz2 mus musculu
24	1152.5	66.2	711	2	Q53TA0_HUMAN	Q53ta0 homo sapien
25	1152.5	66.2	949	2	Q58F15_HUMAN	Q58f15 homo sapien
26	1152.5	66.2	985	1	EPA4B_XENLA	Q91694 xenopus lae
27	1152.5	66.2	986	1	EPHA4_HUMAN	P54764 homo sapien
28	1152.5	66.2	986	2	Q7ZYM7_XENLA	Q7zym7 xenopus lae
29	1152	66.2	986	1	EPA4A_XENLA	Q91845 xenopus lae
30	1151.5	66.1	664	2	Q4RYX7_TETNG	Q4ryx7 tetraodon n
31	1151.5	66.1	983	1	EPHA3_CHICK	P29318 gallus gall
32	1151.5	66.1	986	2	Q5ZEW1_BRARE	Q5zew1 brachydanio
33	1149.5	66.0	983	1	EPHA3_HUMAN	P29320 homo sapien
34	1149.5	66.0	984	2	Q8BRB1_MOUSE	Q8brb1 mus musculu
35	1149.5	66.0	984	2	Q8C3U1_MOUSE	Q8c3u1 mus musculu
36	1145.5	65.8	983	2	Q6P4R6_HUMAN	Q6p4r6 homo sapien
37	1143.5	65.7	993	1	EPHA7_CHICK	O42422 gallus gall
38	1143.5	65.7	998	1	EPHA7_HUMAN	Q15375 homo sapien
39	1142.5	65.6	963	2	Q4RQW0_TETNG	Q4rqw0 tetraodon n
40	1142.5	65.6	984	1	EPHA3_RAT	O08680 rattus norv
41	1142.5	65.6	998	1	EPHA7_RAT	P54759 rattus norv
42	1139.5	65.5	994	2	Q8R381_MOUSE	Q8r381 mus musculu
43	1139.5	65.5	998	2	Q8BSU8_MOUSE	Q8bsu8 mus musculu
44	1135.5	65.2	998	1	EPHA7_MOUSE	Q61772 mus musculu
45	1134.5	65.2	976	2	Q90ZN9_BRARE	Q90zn9 brachydanio

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OM protein - protein search, using sw model

Run on: March 21, 2006, 22:35:54 ; Search time 70.7212 Seconds
                                            (without alignments)
                                            2068.873 Million cell updates/sec

Title: US-10-601-324-3
Perfect score: 1759
Sequence: 1 MSYYHHHHHHDYDIPTTENL..........LKTLADFDPRVSIRLPSTSG 333

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_21:*
                 1: geneseqp1980s:*
                 2: geneseqp1990s:*
                 3: geneseqp2000s:*
                 4: geneseqp2001s:*
                 5: geneseqp2002s:*
                 6: geneseqp2003as:*
                 7: geneseqp2003bs:*
                 8: geneseqp2004s:*
                 9: geneseqp2005s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                   SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1590.5	90.4	456	9	ADZ66216	Adz66216 Primary a
2	1590.5	90.4	456	9	AEB80037	Aeb80037 Human Eph
3	1590.5	90.4	456	9	AEB72924	Aeb72924 Human Eph
4	1590.5	90.4	963	8	ABM83447	Abm83447 Human dia
5	1590.5	90.4	976	7	ADE40423	Ade40423 Human eph
6	1590.5	90.4	976	7	ADJ95092	Adj95092 Novel NOV
7	1590.5	90.4	976	8	ADL61214	Adl61214 Human pro
8	1590.5	90.4	976	8	ADN03964	Adn03964 Antipsori
9	1590.5	90.4	976	9	ADU79818	Adu79818 Human Eph
10	1590.5	90.4	976	9	ADU79822	Adu79822 Human Eph
11	1590.5	90.4	976	9	ADV94805	Adv94805 Human ADP
12	1590.5	90.4	976	9	ADW96093	Adw96093 Human Eph
13	1590.5	90.4	976	9	ADZ66185	Adz66185 EphA2 pol
14	1590.5	90.4	976	9	AEB72892	Aeb72892 Human rec
15	1590.5	90.4	987	8	ADX97538	Adx97538 Pancreati

16	1590.5	90.4	1035	9	ADZ66203	Adz66203 Protein e
17	1590.5	90.4	1035	9	AEB80023	Aeb80023 Human Eph
18	1590.5	90.4	1035	9	AEB72910	Aeb72910 Fusion pr
19	1590	90.4	479	9	ADZ66218	Adz66218 Protein e
20	1590	90.4	479	9	AEB80039	Aeb80039 Human Eph
21	1590	90.4	479	9	AEB72926	Aeb72926 Fusion pr
22	1590	90.4	490	9	ADZ66223	Adz66223 Protein e
23	1590	90.4	490	9	AEB80045	Aeb80045 Human Eph
24	1590	90.4	490	9	AEB72932	Aeb72932 Fusion pr
25	1590	90.4	497	9	ADZ66220	Adz66220 Protein e
26	1590	90.4	497	9	AEB80043	Aeb80043 Human Eph
27	1590	90.4	497	9	AEB80041	Aeb80041 Human Eph
28	1590	90.4	497	9	AEB72928	Aeb72928 Fusion pr
29	1590	90.4	497	9	AEB72930	Aeb72930 Fusion pr
30	1544	87.8	977	9	AEA55026	Aea55026 Mouse tyr
31	1544	87.8	977	9	AEA55035	Aea55035 Mouse eph
32	1201	68.3	710	2	AAR75714	Aar75714 Eph-relat
33	1201	68.3	722	2	AAR75705	Aar75705 Eph-relat
34	1201	68.3	744	2	AAR75713	Aar75713 Eph-relat
35	1199	68.2	877	2	AAW71628	Aaw71628 Mouse Bsk
36	1199	68.2	1041	9	ADV97895	Adv97895 Murine pr
37	1196	68.0	953	5	ABP52826	Abp52826 Human rec
38	1196	68.0	975	5	ABP52827	Abp52827 Human Ehk
39	1196	68.0	991	2	AAR85090	Aar85090 EPH-like
40	1196	68.0	1037	5	ABG61868	Abg61868 Prostate
41	1196	68.0	1037	6	ABR44241	Abr44241 Tyrosine
42	1196	68.0	1037	7	ADE31683	Ade31683 Human 141
43	1191	67.7	928	2	AAR97853	Aar97853 Rat REK7
44	1184	67.3	1005	2	AAW83147	Aaw83147 Rat recep
45	1156.5	65.7	849	2	AAR75706	Aar75706 Eph-relat

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OM protein - protein search, using sw model

Run on: March 21, 2006, 22:46:54 ; Search time 16.7899 Seconds
                                            (without alignments)
                                            1639.734 Million cell updates/sec

Title: US-10-601-324-3
Perfect score: 1759
Sequence: 1 MSYYHHHHHHDYDIPTTENL..........LKTLADFDPRVSIRLPSTSG 333

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_AA:*
                 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
                 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
                 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
                 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                    SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1590.5	90.4	976	1	US-08-449-645A-18	Sequence 18, Appl
2	1590.5	90.4	976	1	US-08-702-367A-18	Sequence 18, Appl
3	1590.5	90.4	976	2	US-09-949-016-6499	Sequence 6499, Ap
4	1590.5	90.4	976	4	PCT-US95-04681-18	Sequence 18, Appl
5	1590.5	90.4	1013	2	US-09-949-016-7991	Sequence 7991, Ap
6	1569.5	89.2	977	1	US-08-673-789-8	Sequence 8, Appli
7	1201	68.3	490	1	US-08-673-789-13	Sequence 13, Appl
8	1201	68.3	710	1	US-08-162-809-22	Sequence 22, Appl
9	1201	68.3	722	1	US-08-162-809-4	Sequence 4, Appli
10	1201	68.3	744	1	US-08-162-809-20	Sequence 20, Appl
11	1199	68.2	877	1	US-08-673-789-2	Sequence 2, Appli
12	1196	68.0	953	2	US-09-751-389-7	Sequence 7, Appli
13	1196	68.0	967	1	US-08-449-645A-30	Sequence 30, Appl
14	1196	68.0	967	1	US-08-702-367A-30	Sequence 30, Appl
15	1196	68.0	975	2	US-09-751-389-8	Sequence 8, Appli
16	1196	68.0	991	1	US-08-449-645A-13	Sequence 13, Appl
17	1196	68.0	991	1	US-08-702-367A-13	Sequence 13, Appl
18	1196	68.0	991	4	PCT-US95-04681-13	Sequence 13, Appl

19	1191	67.7	928	1	US-08-442-248-2	Sequence 2, Appli
20	1191	67.7	928	1	US-08-440-815-2	Sequence 2, Appli
21	1191	67.7	928	2	US-08-486-449-2	Sequence 2, Appli
22	1191	67.7	928	2	US-08-578-684-2	Sequence 2, Appli
23	1184	67.3	1005	1	US-08-469-537A-103	Sequence 103, App
24	1156.5	65.7	849	1	US-08-162-809-6	Sequence 6, Appli
25	1156.5	65.7	986	1	US-08-673-789-3	Sequence 3, Appli
26	1154.5	65.6	849	1	US-08-673-789-10	Sequence 10, Appl
27	1152.5	65.5	986	1	US-08-449-645A-15	Sequence 15, Appl
28	1152.5	65.5	986	1	US-08-702-367A-15	Sequence 15, Appl
29	1152.5	65.5	986	4	PCT-US95-04681-15	Sequence 15, Appl
30	1152.5	65.5	997	2	US-09-949-016-7171	Sequence 7171, Ap
31	1152.5	65.5	1104	1	US-08-222-616-36	Sequence 36, Appl
32	1152.5	65.5	1104	2	US-08-446-648-36	Sequence 36, Appl
33	1152.5	65.5	1104	2	US-09-982-610-36	Sequence 36, Appl
34	1152.5	65.5	1104	4	PCT-US95-04228-36	Sequence 36, Appl
35	1151.5	65.5	968	2	US-09-751-389-6	Sequence 6, Appli
36	1151.5	65.5	983	1	US-08-162-809-16	Sequence 16, Appl
37	1151	65.4	998	1	US-08-449-645A-17	Sequence 17, Appl
38	1151	65.4	998	1	US-08-702-367A-17	Sequence 17, Appl
39	1151	65.4	998	2	US-09-949-016-6501	Sequence 6501, Ap
40	1151	65.4	998	4	PCT-US95-04681-17	Sequence 17, Appl
41	1151	65.4	1005	2	US-09-949-016-9901	Sequence 9901, Ap
42	1149.5	65.3	982	1	US-08-673-789-4	Sequence 4, Appli
43	1149.5	65.3	983	1	US-08-449-645A-21	Sequence 21, Appl
44	1149.5	65.3	983	1	US-08-702-367A-21	Sequence 21, Appl
45	1149.5	65.3	983	2	US-09-771-161A-227	Sequence 227, App

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OM protein - protein search, using sw model

Run on: March 21, 2006, 23:02:20 ; Search time 57.2383 Seconds
                                             (without alignments)
                                             2430.838 Million cell updates/sec

Title: US-10-601-324-3
Perfect score: 1759
Sequence: 1 MSYYHHHHHHDYDIPTTENL..........LKTLADFDPRVSIRLPSTSG 333

Scoring table: BLOSUM62
                   Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_AA_Main:*
                   1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
                   2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
                   3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
                   4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
                   5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
                   6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1590.5	90.4	976	4	US-10-366-288-2	Sequence 2, Appli
2	1590.5	90.4	976	4	US-10-287-226-320	Sequence 320, App
3	1590.5	90.4	976	4	US-10-648-593-138	Sequence 138, App
4	1590.5	90.4	976	5	US-10-616-403-6	Sequence 6, Appli
5	1590.5	90.4	976	5	US-10-897-711-2	Sequence 2, Appli
6	1523.5	86.6	297	5	US-10-794-493-15	Sequence 15, Appl
7	1201	68.3	490	5	US-10-732-923-13669	Sequence 13669, A
8	1201	68.3	827	5	US-10-732-923-13666	Sequence 13666, A
9	1201	68.3	991	5	US-10-732-923-13667	Sequence 13667, A
10	1201	68.3	1013	5	US-10-732-923-13668	Sequence 13668, A
11	1199	68.2	1041	5	US-10-840-512-215	Sequence 215, App
12	1196	68.0	369	5	US-10-732-923-13681	Sequence 13681, A
13	1196	68.0	953	4	US-10-412-277-7	Sequence 7, Appli
14	1196	68.0	975	4	US-10-412-277-8	Sequence 8, Appli
15	1196	68.0	991	3	US-09-823-187-44	Sequence 44, Appl
16	1196	68.0	1037	4	US-10-316-124-3	Sequence 3, Appli
17	1196	68.0	1037	4	US-10-353-690-40	Sequence 40, Appl
18	1196	68.0	1037	6	US-11-064-551-3	Sequence 3, Appli

19	1191	67.7	928	2	US-08-578-684-2	Sequence 2, Appli
20	1185.5	67.4	295	5	US-10-794-493-13	Sequence 13, Appl
21	1184	67.3	1005	4	US-10-029-020-63	Sequence 63, Appl
22	1152.5	65.5	295	5	US-10-794-493-12	Sequence 12, Appl
23	1152.5	65.5	985	4	US-10-029-020-61	Sequence 61, Appl
24	1152.5	65.5	986	5	US-10-723-860-597	Sequence 597, App
25	1152.5	65.5	986	5	US-10-756-149-4880	Sequence 4880, Ap
26	1152.5	65.5	997	5	US-10-450-763-36048	Sequence 36048, A
27	1152.5	65.5	1026	5	US-10-450-763-53290	Sequence 53290, A
28	1152.5	65.5	1104	3	US-09-982-610-36	Sequence 36, Appl
29	1151.5	65.5	968	4	US-10-412-277-6	Sequence 6, Appli
30	1151.5	65.5	983	5	US-10-732-923-13675	Sequence 13675, A
31	1151	65.4	993	3	US-09-823-187-39	Sequence 39, Appl
32	1151	65.4	993	3	US-09-823-187-41	Sequence 41, Appl
33	1151	65.4	998	3	US-09-823-187-40	Sequence 40, Appl
34	1150	65.4	998	3	US-09-823-187-43	Sequence 43, Appl
35	1149.5	65.3	983	3	US-09-771-161A-227	Sequence 227, App
36	1149.5	65.3	983	4	US-10-205-823-97	Sequence 97, Appl
37	1149.5	65.3	983	4	US-10-345-680-2	Sequence 2, Appli
38	1149.5	65.3	983	4	US-10-295-027-602	Sequence 602, App
39	1149.5	65.3	983	4	US-10-029-020-59	Sequence 59, Appl
40	1149.5	65.3	983	5	US-10-794-514A-467	Sequence 467, App
41	1149.5	65.3	983	5	US-10-489-125B-11	Sequence 11, Appl
42	1149.5	65.3	983	6	US-11-051-454-97	Sequence 97, Appl
43	1147.5	65.2	295	5	US-10-794-493-11	Sequence 11, Appl
44	1143.5	65.0	295	5	US-10-794-493-6	Sequence 6, Appli
45	1143.5	65.0	295	5	US-10-794-493-9	Sequence 9, Appli

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OM protein - protein search, using sw model

Run on:          March 21, 2006, 23:03:25 ; Search time 8.14056 Seconds
                                            (without alignments)
                                            1170.855 Million cell updates/sec


Title:           US-10-601-324-3
Perfect score:   1759
Sequence:        1 MSYYHHHHHHDYDIPTTENL..........LKTLADFDPRVSIRLPSTSG 333


Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        169630 seqs, 28622889 residues


Total number of hits satisfying chosen parameters:      169630


Minimum DB seq length: 0
Maximum DB seq length: 2000000000


Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries


Database :       Published_Applications_AA_New:*
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                 2:  /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
                 3:  /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
                 4:  /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
                 5:  /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
                 6:  /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
                 7:  /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
                 8:  /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*


        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.


                                SUMMARIES
                    %
Result             Query
   No.    Score    Match Length DB    ID                      Description
-----------------------------------------------------------------------------
      1  1590.5    90.4     456  6  US-10-966-483-34        Sequence 34, Appl
      2  1590.5    90.4     456  7  US-11-021-441-18        Sequence 18, Appl
      3  1590.5    90.4     976  6  US-10-966-483-2         Sequence 2, Appli
      4  1590.5    90.4     976  6  US-10-511-273-1         Sequence 1, Appli
      5  1590.5    90.4     976  7  US-11-233-796-2         Sequence 2, Appli
      6  1590.5    90.4     976  7  US-11-072-175-138       Sequence 138, App
      7  1590.5    90.4     976  7  US-11-203-251A-77       Sequence 77, Appl
      8  1590.5    90.4    1035  6  US-10-966-483-20        Sequence 20, Appl
      9  1590.5    90.4    1035  7  US-11-021-441-4         Sequence 4, Appli
     10  1590      90.4     479  6  US-10-966-483-36        Sequence 36, Appl
     11  1590      90.4     479  7  US-11-021-441-20        Sequence 20, Appl
     12  1590      90.4     490  6  US-10-966-483-42        Sequence 42, Appl
     13  1590      90.4     490  7  US-11-021-441-26        Sequence 26, Appl
     14  1590      90.4     497  6  US-10-966-483-38        Sequence 38, Appl
     15  1590      90.4     497  6  US-10-966-483-40        Sequence 40, Appl
     16  1590      90.4     497  7  US-11-021-441-22        Sequence 22, Appl
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17	1590	90.4	497	7	US-11-021-441-24	Sequence 24, Appl
18	1196	68.0	1015	7	US-11-203-251A-82	Sequence 82, Appl
19	1196	68.0	1037	7	US-11-203-251A-81	Sequence 81, Appl
20	1184	67.3	1005	7	US-11-113-424-63	Sequence 63, Appl
21	1152.5	65.5	985	7	US-11-113-424-61	Sequence 61, Appl
22	1152.5	65.5	986	7	US-11-203-251A-80	Sequence 80, Appl
23	1151	65.4	998	7	US-11-203-251A-83	Sequence 83, Appl
24	1149.5	65.3	983	7	US-11-113-424-59	Sequence 59, Appl
25	1149.5	65.3	983	7	US-11-203-251A-78	Sequence 78, Appl
26	1118.5	63.6	984	7	US-11-203-251A-85	Sequence 85, Appl
27	1115.5	63.4	984	7	US-11-113-424-60	Sequence 60, Appl
28	1107.5	63.0	987	6	US-10-770-726-61	Sequence 61, Appl
29	1107.5	63.0	987	7	US-11-203-251A-87	Sequence 87, Appl
30	1107.5	63.0	1055	7	US-11-169-041-155	Sequence 155, App
31	1107.5	63.0	1055	7	US-11-072-175-139	Sequence 139, App
32	1107.5	63.0	1055	7	US-11-203-251A-86	Sequence 86, Appl
33	1107.5	63.0	1055	7	US-11-051-720-1417	Sequence 1417, Ap
34	1106.5	62.9	995	7	US-11-113-424-62	Sequence 62, Appl
35	1091.5	62.1	998	6	US-10-510-524-1	Sequence 1, Appli
36	1091.5	62.1	998	7	US-11-203-251A-88	Sequence 88, Appl
37	1090.5	62.0	1035	7	US-11-113-424-20	Sequence 20, Appl
38	1090.5	62.0	1052	7	US-11-113-424-22	Sequence 22, Appl
39	1050	59.7	1005	7	US-11-203-251A-84	Sequence 84, Appl
40	1044.5	59.4	987	6	US-10-949-720-395	Sequence 395, App
41	1044.5	59.4	987	7	US-11-203-251A-89	Sequence 89, Appl
42	1044.5	59.4	990	6	US-10-821-234-1201	Sequence 1201, Ap
43	970	55.1	976	7	US-11-203-251A-76	Sequence 76, Appl
44	772.5	43.9	1006	7	US-11-203-251A-90	Sequence 90, Appl
45	620.5	35.3	258	6	US-10-877-346-75	Sequence 75, Appl

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OM protein - protein search, using sw model

Run on: March 21, 2006, 22:41:59 ; Search time 13.9916 Seconds
                                            (without alignments)
                                            2289.959 Million cell updates/sec

Title: US-10-601-324-3
Perfect score: 1759
Sequence: 1 MSYYHHHHHHDYDIPTTENL..........LKTLADFDPRVSIRLPSTSG 333

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_80:*
                 1: pir1:*
                 2: pir2:*
                 3: pir3:*
                 4: pir4:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1590.5	90.4	976	2	A36355	protein-tyrosine k
2	1551	88.2	426	2	I48759	protein-tyrosine k
3	1544	87.8	977	2	S49004	tyrosine kinase Mp
4	1519	86.4	975	2	I48974	receptor-protein t
5	1201	68.3	490	2	I50613	protein-tyrosine k
6	1201	68.3	1013	2	I50615	receptor-type prot
7	1199	68.2	877	2	I48967	brain-specific kin
8	1196	68.0	991	2	I78843	receptor protein-t
9	1191	67.7	898	2	S47489	receptor tyrosine
10	1184	67.3	893	2	S51603	receptor-like tyro
11	1184	67.3	981	2	S51604	receptor-like tyro
12	1184	67.3	1005	2	S49015	receptor tyrosine
13	1156.5	65.7	849	2	I50617	protein-tyrosine k
14	1153.5	65.6	986	2	S78059	protein-tyrosine k
15	1152.5	65.5	985	2	I51549	receptor tyrosine
16	1152.5	65.5	986	2	I78844	receptor protein-t
17	1151.5	65.5	983	2	B45583	receptor tyrosine
18	1151	65.4	998	2	I58351	receptor protein-t
19	1149.5	65.3	983	2	A38224	protein-tyrosine k
20	1143	65.0	998	2	JC5672	receptor tyrosine

21	1121.5	63.8	983	2	A45583	receptor tyrosine
22	1115.5	63.4	984	2	A39753	protein-tyrosine k
23	1112.5	63.2	952	2	I50612	protein-tyrosine k
24	1107.5	63.0	480	2	I48760	protein-tyrosine k
25	1106.5	62.9	995	2	A56599	embryo kinase 5 -
26	1105.5	62.8	970	2	I78842	receptor protein-t
27	1104.5	62.8	478	2	A57174	protein-tyrosine k
28	1091.5	62.1	948	2	S51605	receptor-like tyro
29	1091.5	62.1	998	2	S37627	protein-tyrosine k
30	1089	61.9	985	2	I51672	receptor tyrosine
31	1088.5	61.9	988	2	I50611	protein-tyrosine k
32	1087.5	61.8	993	2	I48653	mouse developmenta
33	1053.5	59.9	938	2	I49071	protein kinase - m
34	1047	59.5	612	2	S33506	protein-tyrosine k
35	1044.5	59.4	987	2	A54092	protein-tyrosine k
36	1041.5	59.2	987	2	I48953	eph-related recept
37	1035.5	58.9	987	2	I48652	mouse developmenta
38	994.5	56.5	372	2	S23363	protein-tyrosine k
39	974	55.4	1019	2	T13039	tyrosine kinase re
40	942.5	53.6	984	1	A34076	protein-tyrosine k
41	811.5	46.1	919	2	T29581	hypothetical prote
42	799	45.4	1122	2	T42400	Eph receptor tyros
43	772.5	43.9	1006	2	JC5526	kinase-defective E
44	724	41.2	275	2	I48761	protein-tyrosine k
45	633.5	36.0	334	2	T43450	hypothetical prote

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OM protein - protein search, using sw model

Run on: March 21, 2006, 22:37:09 ; Search time 74.2827 Seconds
                                            (without alignments)
                                            3162.796 Million cell updates/sec

Title: US-10-601-324-3
Perfect score: 1759
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Scoring table: BLOSUM62
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Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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                 Listing first 45 summaries

Database :   UniProt_05.80:*
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                 2: uniprot_trembl:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	
1	1590.5	90.4	976	1	EPHA2_HUMAN	P29317	homo sapien
2	1590.5	90.4	976	2	Q8N3Z2_HUMAN	Q8n3z2	homo sapien
3	1544	87.8	977	1	EPHA2_MOUSE	Q03145	mus musculu
4	1424.5	81.0	974	2	Q6DII4_XENTR	Q6dii4	xenopus tro
5	1412.5	80.3	963	2	Q5FWW9_XENLA	Q5fww9	xenopus lae
6	1407.5	80.0	976	2	Q6NTV5_XENLA	Q6ntv5	xenopus lae
7	1355	77.0	977	2	Q9PWR5_XENLA	Q9pwr5	xenopus lae
8	1309.5	74.4	712	2	Q4SC90_TETNG	Q4sc90	tetraodon n
9	1278.5	72.7	1042	2	Q4RXA0_TETNG	Q4rxa0	tetraodon n
10	1246.5	70.9	666	2	O73876_BRARE	O73876	brachydanio
11	1246.5	70.9	984	2	Q6NZS1_BRARE	Q6nzs1	brachydanio
12	1201	68.3	1013	1	EPHA5_CHICK	P54755	gallus gall
13	1199	68.2	877	1	EPHA5_MOUSE	Q60629	mus musculu
14	1196	68.0	369	2	Q95K57_MACFA	Q95k57	macaca fasc
15	1196	68.0	819	2	Q6PFV6_MOUSE	Q6pfv6	mus musculu
16	1196	68.0	1017	2	Q59FT4_HUMAN	Q59ft4	homo sapien
17	1196	68.0	1037	1	EPHA5_HUMAN	P54756	homo sapien
18	1188	67.5	969	2	Q7Z3F2_HUMAN	Q7z3f2	homo sapien
19	1184	67.3	1005	1	EPHA5_RAT	P54757	rattus norv
20	1156.5	65.7	986	1	EPHA4_CHICK	Q07496	gallus gall
21	1153.5	65.6	927	2	Q99KA8_MOUSE	Q99ka8	mus musculu
22	1153.5	65.6	986	1	EPHA4_MOUSE	Q03137	mus musculu

23	1153.5	65.6	986	2	Q80VZ2_MOUSE	Q80vz2	mus musculu
24	1152.5	65.5	711	2	Q53TA0_HUMAN	Q53ta0	homo sapien
25	1152.5	65.5	949	2	Q58F15_HUMAN	Q58f15	homo sapien
26	1152.5	65.5	985	1	EPA4B_XENLA	Q91694	xenopus lae
27	1152.5	65.5	986	1	EPHA4_HUMAN	P54764	homo sapien
28	1152.5	65.5	986	2	Q7ZYM7_XENLA	Q7zym7	xenopus lae
29	1152	65.5	986	1	EPA4A_XENLA	Q91845	xenopus lae
30	1151.5	65.5	664	2	Q4RYX7_TETNG	Q4ryx7	tetraodon n
31	1151.5	65.5	983	1	EPHA3_CHICK	P29318	gallus gall
32	1151.5	65.5	986	2	Q5ZEW1_BRARE	Q5zew1	brachydanio
33	1151	65.4	993	1	EPHA7_CHICK	O42422	gallus gall
34	1151	65.4	998	1	EPHA7_HUMAN	Q15375	homo sapien
35	1150	65.4	998	1	EPHA7_RAT	P54759	rattus norv
36	1149.5	65.3	983	1	EPHA3_HUMAN	P29320	homo sapien
37	1149.5	65.3	984	2	Q8BRB1_MOUSE	Q8brb1	mus musculu
38	1149.5	65.3	984	2	Q8C3U1_MOUSE	Q8c3u1	mus musculu
39	1147	65.2	998	2	Q8BSU8_MOUSE	Q8bsu8	mus musculu
40	1145.5	65.1	983	2	Q6P4R6_HUMAN	Q6p4r6	homo sapien
41	1143	65.0	998	1	EPHA7_MOUSE	Q61772	mus musculu
42	1142.5	65.0	963	2	Q4RQW0_TETNG	Q4rqw0	tetraodon n
43	1142.5	65.0	984	1	EPHA3_RAT	O08680	rattus norv
44	1142	64.9	994	2	Q8R381_MOUSE	Q8r381	mus musculu
45	1139	64.8	976	2	Q90ZN9_BRARE	Q90zn9	brachydanio